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Ouery Score Match Length DB ID	100.0 1031 6 32.7 18207 9 29.7 191750 2 20.9 191750 2 20.9 230755 2	185.2 18.0 15597 3 APO74901 183.4 17.8 182211 9 AL360004 108.4 10.5 41345 3 CEF15G9 93.6 9.1 1610 9 HSA24418 91.4 8.9 4312 10 AF134319 89.4 8.7 157029 9 AL135796 69.8 6.8 87461 9 HSA21996	6.8 180248 9 6.3 717 11 6.0 356 11 5.0 1873 3 4.9 2336 3	4.9 2338 6 4.9 4359 10 4.7 87810 2 4.6 154137 8 4.6 41173 1	4.5 3867 1 4.5 1026 3 4.3 43349 1 4.3 4377 10	4.3 12606 1 4.2 18023 1 4.2 18023 6 4.2 87810 2 4.2 87810 2 4.2 2745 6	4.2 2047 4.2 5991 4.2 6423 4.2 198677 4.1 132470	2.4 4.1 12356 10 2.4 4.1 135545 10 2.4 4.1 13545 10 2.2 4.1 100000 9 2.2 4.1 125350 2	ALIGNMENTS	AX108634 1031 bp DNA Sequence 2 from Patent W00123419. AX108634 AX108634.1 GI:13923866	Norway rat. Rattus norvegicus Eukaryota; Metazoa; Mammalia; Eutheria;	Construction of the control of the c
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: March 7, 2002, 18:47:47 ; Search time 1988.65 Seconds (without alignments)	Title: US-09-665-728-2 Perfect score: 1031 Sequence: 1 tctagcgaaccccttcggccagcccggctcgagcgccgc 1031 Scoring table: IDENITY	d: 1472140 seqs, 824855 umber of hits satisfying chose DB seq length: 0	Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45.	DEMbl: gb_ba gb_ht gb_in	4: gb_om:* 5: gb_ov:* 6: gb_pat:* 7: gb_ph:* 8: gb_ph:* 9: qb_ph:*	10: gb_ro:* 11: gb_ss:* 12: gb_sy:* 13: gb_un:* 14: gb_v1:* 15: em ha:*			25: em_ro:* 27: em_sts:* 27: em_sy:* 28: em_un:* 39: em_higo_hum:* 31: em_higo_hum:* 32: em_higo_hum:*	33: em_htg_lton:* 34: em_htg_lton:* 34: em_htg_ltor:* 35: em_htg_rod:* 36: em_htg_rod:*	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. \$ SUMMARIES

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,
Dederlch, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pacce, A., Williams, G., Bonnih, D., Brooks, A.,
Buhay, C., Burket, C., Chacko, J., Chen, G., Chen, S.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferragutch, Forcum-Tansey, J., Glll, R.,
Gorrell, J. H., Gunratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mel, G., Moore, S., Morgan, M., Martin, R.,
Nallamson, A., Wrensford, G., Moure, N., Oguh, M., Parish, B.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Wallington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.W., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Worley, K. and Gibbs, R.
Direct Submission

NL Unpublished
2 (bases 1 to 191750)

NL Submitted (24-FEB-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Jan 4, 2001 this sequence version replaced gi:11096415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 29 contist. The true order of the pieces is not known and their order in this sequence record is
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Sequencing vector: M13: L08821
Chemistry: Dye-primer Bodipy: 74% of reads
Chemistry: Dye-terminator B14 Dye: 26% of reads
Assembly program: Phrap; version 0.993329
Consensus quality: 159536 bases at least 040
Consensus quality: 173428 bases at least 030
Consensus quality: 179682 bases at least 020
Estimated insert size: 180449; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: MABZ
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Center code: BCM
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                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Museria; Rodentia; Sciurognathi; Muridae; Murinae; Museria; Lo 191750)

I (bases 1 to 191750)

Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C., Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T., Addison,S., Pacce,A., Williams,G., Bondin,D., Brooks,A., Brown,J., Buhay,C., Burket,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hoques,M., Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hoques,M., Kovar,C., Liu,J., Liu,W., Loulseged,H., Vargan,M., Martin,R., Massey,E., McLedd,M.P., Mel,G., Moore,S., Morgan,M., Martin,R., Malliamson,A., Mrensford,G., Mouyen,N., Oguh,M., Parish,B., Perez,L., Reilez,D., Say,J., Sheh,H., Vasquez,L., Watlington,S., Wulliamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Worley,K. and Gibbs,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 4, 2001 this sequence version replaced gi:11096415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jenuel Council and Statistics
Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 74% of reads
Chemistry: Dye-terminator B19 Dye: 26% of reads
Chemistry: Dye-terminator B19 Dye: 26% of reads
Assembly program: Phrap; version 0.990329
Consenus quality: 15956 bases at least Q40
Consensus quality: 173428 bases at least Q30
Consensus quality: 173682 bases at least Q30
Estimated insert size: 180449; sum-of-contigs estimation
Quality coverage: Ox in Q20 bases; sum-of-contigs estimation
Quality coverage: 3.2x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (see http://www.hgsc.bcm.tmc.edu/docs/Genbark_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                   ACO24113 191750 bp DNA HTG 07-JAN-2001 Mus musculus chromosome 11 clone RP23-277F6, WORKING DRAFT SEQUENCE, 29 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
DD 191408 TCATCGCCAACTATGCGCTGGTGCCTTTCCACGACCCAGGTAGAGCCCC 191456
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19980: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.hgsc.bcm.tmc.edu/
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Center code: BCM
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Mus musculus, clone RP23-22C1

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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Boyuslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G.,

Rodge, S., Donlano, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,

Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S.,

Dodge, S., Donlano, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,

Galagan, J., Gardyna, S., Glinde, S., Goyette, M., Graham, L.,

Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,

Klein, J., LaRocque, K., Lamacares, R., Landers, T., Lehoczky, J.,

Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N.,

McZarthy, M., McEwan, P., McGurk, A., McKernan, K., Peterre, R.,

Mrphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

O'Neil, D., Ollvar, T.M., Ollver, J., Peterson, K., Pterre, N.,

Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,

Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,

Voung, G., Zainoun, J., Zimmer, A. and Zody, M.

Sailtev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,

Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Smit, A.F.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 230755)
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Mus musculus clone RP23-22C1, WORKING DRAFT SEQUENCE, 45 unordered
                                                                                                                                                                                                                                                                                                                                                                                    13479 ACCATGAGGAGGAGGGCGACCACACACAGAATCCCCTTTGACCCCCAGCCTGAAGGAGG 13420
                                                                                                                                                           13419 TCACCATTGCACTGAGCGGACCAGGGCCTGAGATTGAAGTCCGGGACCCACTGGGTATGT 13360
                                                                                                                                                                                                                                                                                                                       13359 GCCCCAGGGCTCACCTCTTTGGATACAAGACTGAGCTGAGAGACAAAAGATGAG 13300
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Center: Whitehead Institute/ MIT Center for Genome Research
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tcaccatctcactgagcgggccagggcctgagatcgaagtccgggacccactgggtatgt
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Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center project Information
Center project name: L5311
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AC024618.2 GI:10280861
HTG; HTGS_PHASE1; HTGS_DRAFT.
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arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                        Chemistry: Dye-terminator Big bye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 206138 bases at least Q40 consensus quality: 218628 bases at least Q30 consensus quality: 223560 bases at least Q20 Insert size: 226355; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2865 2964: gap of 100 bp 1n length 2865 2964: gap of 100 bp 2965 4029: contig of 1065 bp in length 4030 4129: gap of 100 bp 4130 5611: contig of 100 bp 5712 6711: gap of 100 bp 1n length 5712 6811: contig of 100 bp in length 6812 6811: contig of 100 bp 6812 6813: gap of 100 bp 10 length 6713: gap of 100 bp 100 
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Center clone name: 22_C_1
------ Summary Statistics
Sequencing vector: M13; M77815; 100% of reads
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26126: contig of 2660 bp in length
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7559: contig of 4922 bp 1n 197: gap of 100 bp 1n 1905: contig of 4308 bp 1n 105: gap of 100 bp
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14005: contig of 1892
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us-09-665-728-2.rge

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169638 1669737; gap of 100 bp 169738 178139; contig of 8402 bp in length 178140 178239; gap of 100 bp 18840 178239; gap of 100 bp 178240 188969; contig of 100 bp 188970 189069; gap of 100 bp 198835; contig of 9766 bp in length 198836 198935; contig of 12565 bp in length 198836 211500; contig of 12565 bp in length 211501 211600; gap of 100 bp 211501 214265; contig of 12565 bp in length 224457 224456; gap of 100 bp 224555; contig of 6229 bp in length 10. 230755; contig of 6229 bp in length.
                                                                                     97689 97788 9ap of 100 bp
97789 102663: contig of 4875 bp in length
102664 102763: gap of 100 bp
102764 12018: contig of 17255 bp in length
2019 125200: contig of 500 bp
                                                                                                                                                                              120119 125200: contig of 5082 bp in length 125201 125300: gap of 100 bp 125301 13132: contig of 6032 bp in length 13133 131432: gap of 100 bp 131433 137931: contig of 6499 bp in length 131433 138033: gap of 100 hp
               87008: gap of 100 bp
93267: contig of 6259 bp in length
93367: gap of 100 bp
97688: contig of 4321 bp in length
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26227. 29160
/note="assembly_fragment"
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/gene="him-4"
/note="mutants have defects in cell adhesion and germ-line
chromosome segregation"
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Caenorhabditis elegans hemicentin precursor (him-4) mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemicentin, a conserved extracellular member of the immunoglobulin superfamily, organizes epithelial and other cell attachments into oriented line-shaped junctions
Development 128 (6), 883-894 (2001)
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Vogel.B.E. and Hedgecock,E.M.
Direct Submission
Submitted (25-UN-1998) Biology, Johns Hopkins University, 3400 N.
Charles St., Baltimore, MD 21218, USA
Location/Qualifiers
1. 15597
/organism="Caenorhabditis elegans"
/strain" Bristol N2"
                                                                                                                                                                                                                                                                                                 DD 112006 AGGTGTTAAAGTGGGTGGAGTCAGCAATCCAGGCCTCCAAAGTTCATCTGCTGTGTGCAG 112065
                                                                                                                                                                                                                                                                                                                                                                       889 --cccagggttcacctcctcttctgatgcaagactgagctggaag----gccaggctgag 942
                                                                                                                                                         709 aggtgttaaagtgggtggagtccgcatccaggcctccaaagttcatctgctgtcagcag 768
                                                                                            Length 230755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota, herazoa, Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                            Indels
                                                                                       Query Match 20.9%; Score 215.8; DB 2; Best Local Similarity 84.8%; Pred. No. 4.7e-34; Matches 267; Conservative 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /chromosome="X"
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29261. .33742
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33843. .37207
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Vogel, B.E. and Hedgecock, E.M.
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AF074901.1 GI:3328185
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AUTHORS
TITLE .
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KEYWORDS
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AF074901
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LPPPVRLWTYEGEKIDSQLIPHTIREDGALVLONVKLENTGVFVCQVSNLAGEDSLSY
TLTVHEKPRIISEVPGVVDVVKGFTIEIPCRATGVPEVIRTWNKNGIDLKMDEKKFSY
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BVLCTLRISEADKNDIGNNVVYNTRAGTSQMTHVDVQEPPIILPSYGTNNTRAVGD
RVLCYVEXEXPSPASVTWFRKGIAIGTDTKGYVVESDGTLVIQSASVEDATITCKAS
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PLIDDKTSWKTSDDKRKLHVFKAKITDSGVYKCVARNAAGEGSKSFQVEVIVPLED
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DSVSVKQEGNYHCVAQSKGNILDIDVELSVLAVPIVGEDDNLEVFLGKDISLSCDLQT
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TLTLDLVLEPWYSVEPVFFANNKLIGNNPIILQCQYTGNPKPTVIWKIDGNDVDKSWLF
DESLELRIEKLTGKSAQISCTABNKAGTASRRPFIQNIAAPPFKNEGDQETIFRESE
TITLDCPVSLGDFQITWMKQGLPLTENDAIFTLDNTRLTILNANRDHEDIYTCVANNT
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RRLTILNVTENDEGQYSCRVKNDAGENSFDFKATVLVPPTIIMLDKDKNKTAVEHSTV
TLSCPATGKPEPDITWFKDGEAIHIENIADIIPNGELNGNQLKITRIKEGDAGKYTCE
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GKPLQSDKFVKTSANGQKLYLFKLRETDSSKYTCIATNEAGTDKRDFKVSMLVAPSFD
EPNIVRRITVNSGNPSTLHCPAKGSPSPTITWLKDGNAIEPNDRYVFFDAGRQLQISK
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VARODTMLTCTCNAESSYVEHANDESVONGYTTSKAABKTLWTNIQLDDE
GFYYCTANNEAGITKFFKLIVIETPYFLDQOKLYPILGKRLTLOCSANGTPPPTL
FMKDGKRLNESDEVDIIGSTLVIDNPQKEVEGRYTCIAENKAGRSEKDMAYEVLLDPR
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QATPEDADSYSCIAVNDAGGAEAVFQVTVNTPPKIFGDSFSTTEIVADTTLEIPCRTE
GIPPPEISWFLDGKPILEMPGVTYKQGDLSLRIDNIKPNQEGRYTCVAENKAGRAEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTIDLKNVKLIRLKDPSPGVWTVNTNSRLKHTIRVFGHGAVDFKYGFASRPLDRIEL
ARPRPVLNQDTYLLINMTGLIPPGTVGEIDLVDYHGHSLYKAVASPHRTNPNMYFAGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AMSQAGQARDTTDLMLATPPKVEIIONKMWCRGDRVSFECKTIRGKPHPKIRWFKNG
KDLIKPDDYIKINEGQLHIMGAKDEDAGAYSCVGENMAGKDVQVANLSVGRVPTIIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PHTVRVNIERQYTLQCLAVGIPPPEIEWQKGNVLLATLNNPRYTQLADGNLLITDAQI
EDQGQFTCIARNTYGQQSQSTTLMVTGLVSPVLGHVPPEEQLIEGQDLTLSCVVVLGT
PKPSIVWIKDDKPVEEGPTIKIEGGGSLLRLRGGNPKDEGKYTCIAVSPAGNSTLHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VQLIKKPEFVYKPEGGIVFKPTISGMDEKHVAVVNSTHDVLDGEGFAIPCVVSGTPPP
IITWYLDGRPITPNSRDFTVTADNTLIVRKADKSYSGVYTCQATNSAGDNEQKTTIRI
MNTPMISPGQSSFNMVVDDLFTIPCDVYGDPKPVITWLLDDKPFTEGVVNEDGSLTIP
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EAVFVNNNHTVVVNNVTKYHTGVYKCYATNKVGQAVKTINVHVRTKPRFESGLTESEL
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SYACTVTNEAGVATKTFNLFVQVPPTIVNEGGEYTVIENNSLVLPCEVTGKPNPVVTW
TKDGRPVGDLKSVQVLSEGQQFKIVHAEIAHKGSYICMAKNDVGTAEISFDVDIITRP
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RKLFDFAVNDPPSISDĒLSSANIQTIVPYYPVEINCVVSGSPHPKVYWLFDDKPLEPD
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GDTLMILKAQRFDGGLYTCVATNSYGDSEQDFKVNVYTKPYIDETIDGTPKAVAGGEI
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GNLTTHYAAEVIGKPTFVRKGGNLYEVIENDTITMDCGVTSRPLPSISWFRGDKPVYL
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                                                                                                                                                                                                                                                                               /translation="MGRSPSWLYGVLGLLLLATTCSSVNDDKNDPTGKSSLAFVFDIT
GSMFDDLVQVREGAAKIFKTVMAQREKLIYNYIMVPFHDPYLGEIINTTDSTYFWRQL
                                                                                                                                                                                                                                                                                                                                                                                             SKVYVHGGGDCPEKTLTGILKALQISLPSSFIYVFTDARSKDYHLEDEVLNTIQEKOS
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TVESASAYTIYWVKTGEDIIGGPLFYHNTDTSVWTIPELSLKDAGEYECRVISNNGNY
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/note="alternatively spliced form has been detected"
                                                                                                       /product="hemicentin precursor"
/protein_id="AAC26792.1"
/db_xref="GI:3328186"
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YODI IS WILLIAM TRANSAROTI I I DATA TO THIS TO THE TO THE TOTAL TO
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HEGSANDDGFGPTTQDSLFEFNPPLHPEISVVNTDCAGTINENGDCVDKDGKTHNLKI
LTGENHCPEGFAMNPHTRICEDLDECAFYQPCDFECINYDGGFQCNCPLGYELAEGG
RDVNECESVRCEDGRACFUNDGGFECINYDGGFQCNCPLGYELAEGG
HAVNECSPYCEDGRACFUNDGGFECINDPCPANYSLVDDRYCEPECTSTPIQVH
MLAIPSGLPISHITATLAYDKSGRVLMDTTVAISDFGAPLARGRMTSGPFTIKAVKRG
HAQVWTNRVLAAGDHHKVRVRAHSDHATNELHAPKETNFLVLINVGQYPF"
                                    ISNGGTKQVIEGELAVIECLVEGYPAPQVSWLRNGNRVETGVQGVRYVTDGRMLTIIE
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                                                                    ARSLDSGIYLCSATNEAGSAQQAYTLEVLVSPKIITSTPGVLTPSSGSKFSLPCAVRG
NGTALTHSTPGITVASDSTFIQINNVSLSDKGVYTCYAENVAGSDNLMYNVDVVQAPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note-"48 tandem repeats; Region: immunoglobulin repeats" 14842. 14985
/gene-"him-4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 tetgatgeaggtgategaeggegeeteaegeattetggagegeagtetgageageegeag 313
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/4986. 15099
/gene-"him-4"
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nes 293;
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0; Mismatches
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15100. .15228
/gene="him-4"
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55.2%; Pred. No. 1.36
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3228 c 3417 g 4003
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1300. 14544
/gene-"him-4"
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Lubrited (16-AUG-2001) Sanger Centre, Hinxton, cambridgeshire, Submitted (16-AUG-2001) Sanger Centre, Hinxton, cambridgeshire, CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requestis: clonerquest@sanger.ac.uk

On Aug 18, 2001 this sequence version replaced gi:15020463.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality)=

30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one MI3 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr:, TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at the sequence of the sequence o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RP11-18617 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL360004 182211 bp DNA PRI 16-AUG-2001
Human DNA sequence from clone RP11-88G17 on chromosome 9, complete
sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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This sequence is the entire insert of clone RPI1-88G17 The true right end of clone RPI1-202H3 is at 75398 in this sequence.
Location/Qualifiers
                                                                                                                                                                                                                           629
614 cggtgaccgcacccaccctggctacctggcttttgaggagatcgcctccaccagttctgg 673
                                                                                                                                                                                                                                                                                                        734 catccaggcctccaaagttcatctgctgtcagcagaccacgaggaggagggggaacacac 793
                                                                     510 TGGTAATAGAACACCATCCAGGATTCCGTACATATGAAAAATCGCCGCTGCATCTTTTGG
                                                                                                                                                  674 ccaagtgttccagctggacaagcagcaggtgtcggaggtgttaaagtggggtggagtccgc
                                                                                                                                                                                                       630 TGTCAAACAGAAGAAGTTCATTTGATGTACGAGGCACGTGAACGGGGAGGAACAGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .182211
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/db_xref="taxon:9606"
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/clone="RP11-88G17"
/clone_lib="RPCI-11.1"
43597. .44209
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Kimberley, A.
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misc_feature

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Direct Submission

Submitted (24-DEC-1994) Nematode Sequencing Project, Sanger Centre, Submitted (24-DEC-1994) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CEB10 1RQ, England and Department of Genetics, Washington University, St. Louis, WO 63110, USA. E-mail: jes@sanger.ac.uk or rw@nematode.wustl.edu Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.

Current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones. Exceptions are indicated by an explicit note.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db 137293 CAGAGCCGCGCTCGGCATGATGCCCGGGGCGCCCTCCTGCGGGCTGCTGACCGCGGTCTC 137352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 137353 TGCGGCAGTGGCAGTGGCAGTGGCC---GGGGCGCCCGGGACGGTAATGCCCCCCACCAC 137409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Db 137410 GGGGGACGCCACCTGGCCTTCGTCTTCGACGTCACCGGCTCCATGTGGGACGACTGAT 137469
                                                                                                                                                                                                                                                                                                                                                                                               80 cagectecggeteageatgacgeetagggegeageteetgeegetgeteetggggaeeta 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       140 cacagtagtggcggcggcggtcacatctgatgagcccacgaagacgctgtcccccgccac 199
                                                                                                  /note="Tandem repeat. Forced join. Gap sized to be approximately 150pp from restriction digest data and spanning pUC clone." 47059 c 48127 g 46657 t
                                                                                                                                                                                                                                                                                                                                           Gaps
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HTG; Fibronectin. type III repeat; Transfer-RNA; tRNA-Ala. Caenorhabditis elegans. Caenorhabditis elegans. Caenorhabditis alegans. Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
'note="Sequence from AC006241 sequenced by WIBR"
                           50279. 50351
Anote "Sequence from AC006241 sequenced by WIBR"
9331
                                                                                                                                                                                                                                                                                       Length 182211;
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                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                       Query Match 17.8%; Score 183.4; DB 9; Best Local Similarity 77.4%; Pred. No. 1.5e-27; Matches 236; Conservative 0; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The C.elegans Sequencing Consortium. 2 (bases 1 to 41345)
Sulston, J.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 41345) none.
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IMPORTANT: This sequence is not the entire insert of clone F15G9. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true left end of clone F15G9 is at 1 in this sequence. The true sequence 247070.

The true left end of clone T09B9 is at 41245 in this sequence. The true left end of clone T09B9 is at 8835 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence
                                                                                                                                                                                                                                                                                                                                                                   The end of this sequence (41245. .41345) overlaps with the start of sequence 247070. For a graphical representation of this sequence and its analysis see: _http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
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EETVDAPREVLGESQISDFVEEDDOGTSVEEVKTLTASEPESEEBEEDEDBOWKAQE
LLAAASTOIRESSPVSSPVKRVSSAASLFANDNGWFTENRTPSPTVJAAKKLGGIPWPP
KSSDVKKEGGDAEALPKKRVSDLIARFNTGVVEESKKTDDAYKNEYGAGTNVGKVSTH
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Complement(join(6076. 6174,6498. 6562,6959. 7029,
7077. 7256,7305. 7378))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cloure=#120973. .3089,3208. .3273,3480. .3823,3869. .3947,4131. .4264)
/gene=*F1569.1a*
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/note=*CDNA EST yk102e12.3 comes from this gene CDNA EST yk102e12.5 comes from this gene CDNA EST yk102e12.5 comes from this gene CDNA EST yk16Bh5.3 comes from this gene CDNA EST yk16Bh5.3 comes from this gene CDNA EST yk26C66.3 comes from this gene CDNA EST yk46Bc5.5 comes from this gene CDNA EST yk26Bq4.5 comes from this gene CDNA EST yk26Bq4.5 comes from this gene CDNA EST yk252c2.3 comes from this gene CDNA EST yk252c2.3 comes from this gene CDNA EST yk252c3.3 comes from this gene CDNA EST yk2540.3 comes from this gene CDNA EST yk558g5.3 comes from this gene CDNA EST yk558g5.3 comes from this gene CDNA EST yk58g11.3 comes from this gene **
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Join(3213. .3273,3480. .3823,3869. .3947,4131. .4264)
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/077. .7256,7305. .7378))
/condon_start=1
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CDNA EST yk55895.5 comes from this gene
CDNA EST yk584911.5 comes from this gene"
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1. 41345
//organism="Caenorhabditis elegans"
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/ (Percellide"-CARDAT313.1"

/ (De_xreft="611397595" |
/ (De_xreft="611595" |
/ (De_xreft="61595" |
/ (De_xref
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                                                                                                                                                                                                           Biochemistry, MRC
                      histocompatibility complex, including the gene encoding the casein
kinase II beta subunit (CSNK2B)
Genomics 36 (2), 240-251 (1996)
                                                                                                                                            2 (bases 1 to 1610)
Albertella,M.R.
Thesis (1997) University of Oxford, Department of Biochemistry, MR Immunochemistry Unit
3 (bases 1 to 1610)
Snoek,M., Albertella,M.R., van Kooij,M., Wixon,J., van Vugt,H., de Groot,K. and Campbell,R.D.
G7C, a novel gene in the mouse and human major histocompatibility complex class III region, possibly controlling lung tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           major histocompatibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 acgetgteeceegecacaggagacgecacetggeettegtettegatgteaceggetee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24 AGGCTGCTGGACATCACCCCAGCCTCAGCTTTGTCCTGGACACCACGGGCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3;
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52.8%; Pred. No. 5.2e-09;
tive 0; Mismatches 199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the
                                                                                                                                                                                                                                                                                                                                                                                                                          susceptibility
Immunogenetics 51 (4-5), 383-386 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (02-AUG-1999) Aguado B.,
Genome Campus, Hinxton, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome Campus, Hinxton, Cambridge,
Location/Qualifiers
1.1610
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /map="6p21.3"
/note="class III region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="G7c"
<1. .>1610
/gene="G7c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 (bases 1 to 1610)
Aguado, B.
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1. .1610
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Matches 226; Conservative
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MEDLINE
REFERENCE
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                                                                                         JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /LTAIR 14 LION = MANSEPSKHIZGYLGLLLLATTCSSVNDDKNDPTGKSSLAFVFDIT
GSMFDDLVQVREGAAK IFKTWAQREKLITNNY IMVPFHDPYLGEI INTTDSTYFMROL
SKVYVHGGGDCPEKTLIGILKALQISLPSFTIYVFTDARSKDYHLEDEVLNTIQEKQS
SVVFWYTGDCCARFTHFGFRYTERIAAASFGQVFHLEKSBVSTYLEYVRHAVKQKKVHL
MYEARERGGTVSRNIPVDKHLSELTISLSGDKDDSDNLDIVLRDPEGRTVDKRLYSKE
GGTIDLKNYKLIRLRDPSFGWTVNYNSRLHHTTRYFGHGANDFKYGFASRPLDRIEL
ARPRPVLNQDTYLLINTWTGIL PGFTVGEIDLVDYHGHSLXRAVBSPHRTNPNNYFAGF
FVPPKGLFFVRVQGYDEDNYEFMRIAPTAIGSVIVGGPRAFMSPIHQEFVÖRDLLSC
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Albertella,M.R., Jones,H., Thomson,W., Olavesen,M.G. and Campbell,R.D.
Localization of eight additional genes in the human major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSA245418 1610 bp mRNA PRI 04-MAY-2000 Homo sapiens mRNA for G7c protein (G7c gene located in the class AIZ45418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15823 TTAGAATATGTCAGACATGCTGTCAAACAGAAGAAAGTTCATTTGATGTACGAGGCACGT 15882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15583 GCACTTCAAATTTCCTTACCGTCCTCATTCATTATGTGTTCACTGATGATGAAG 15642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15703 TTCGTGATGACTGGTGACTGTGGTAATAGAACACATCCAGGATTCCGTACATATGAAAA 15762
                                                                                                                                                                                                                                                                        /note="contains similarity to Pfam domain: PF00047 (Immunoglobulin domain), Score=1411.6, E-value=0, N=47 cDNA EST yk556f1.5 comes from this gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ategeeteceaceagttetggeceaagtgtteceagetggaeaageageaggtgteggaggtg 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ttaaagtgggtggagtccgccatccaggcctccaaagttcatctgctgtcagcagaccac 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       534 gactaccacaagaagaatgagctcctgcagctcctgcagctgaagcagtcgcaggtggtc 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              474 gccgtggaggttgccaaccccggctccttcatctacgtcttctcggatgcccgtgccaag 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 41345;
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Z47070.1:2834. 3265,Z47070.1:3313. 3426,
Z47070.1:3882. 4289,Z47070.1:4333. 4473,
Z47070.1:4523. 4666,Z47070.1:4712. 4837,
Z47070.1:4944. 5332,Z47070.1:5571. 6141,
Z47070.1:6349. 6539,Z47070.1:5571. 6141,
Z47070.1:7235. 7444,Z47070.1:7972. 8171)
/gene=FF1569.4a"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 108.4; DB 3; Length
Pred. No. 2.3e-12;
0; Mismatches 166; Indels
                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAA87336.1"
/db_xref="G1:3875956"
/db_xref="SPTREMBL:076518"
                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
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G7c gene; G7c protein.
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Best Local Similarity 55.6%;
Matches 208; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atctcactgagcgg 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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HSA245418
LOCUS
DEFINITION
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KEYWORDS
SOURCE
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PEMCLSALELALHTPPLSDIFVETDASPKDALLTNNYGETBERGRUTFLYTTEDDS
TGGRRRREALSPLENEPERTARASGGEVIETKDOVIQDVAJIVESSLAGGLYTFLYTEDDS
PPVFTPGEPCYPSVDSLLMQYVVRMHDISSFWIKSPAGVSQGPEGGIGPLGHTRRFG
OFWTYTMTDPPRTGELWOODAGTSLDFLFHGISVEDGPHGLYPLT
OFWTYTMTDPPRTGELWOOGOPOFSHYVLRRYPETTOLGRYSLEPVGPPVRG
LLAASLPPTLLSVSSPFSLELWOOGGGESLRTAPOPCSVAVELLELSGPPPKTPG
SKAPLSHYFSFSGPOLLLTTSVNPSFSLTSNLSRARLGINESAMGRLMLEVPDSAA
PSTVTTQRAGGGAAGGCANGTVLAGOSSKDOLDGPAHSAAPVLPPDSAA
PSTVTTQRAGGGAAGGCANGTVLLGGCTSW"
                                                                                                                                                                                                                                                                    /note="exons around recombinational hot spot; corresponds to sequence presented in Genbank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AL135796 157029 bp DNA PRI 27-SEP-2000 Human DNA sequence from clone GS1-164L12 on chromosome 1 Contains an SYS and GSSs, complete sequence.
AL135796.6 GI:7706886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 157029)
Donnelly, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1300 GGCCCCGTCTTTACAACCAGCGACCCGGACAGCTTTTGGCAGAAACTCAACGAGATCCAT 1359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1420 CACACCCCTCCCCTCTGACATCTTTGTCTTCACTGATGCCTCACCCAAGGATGCTCTT 1479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1480 CITACCAACCGGGTGGAATCCCTGACTCGGGAGGGCGCTGCAGGGTGACATTCTAGTA 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 acgotycocccgccacaggagacgccacctggccttcgtcttcgatgtcaccggctcc 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     303 agcagcogcagcoggtcatcgccaactatgcgctggtgcctttccacgacccagacatt 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 atgtgggacgatctgatgcaggtgatcgacggcgcctcacgcattctggagcgcagtctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 gttgccaacccggctccttcatctacgtcttctcggatgcccgtgccaaggactaccac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            543 aagaagaatgagctcctgcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.9%; Score 91.4; DB 10; Length 4312; 52.4%; Pred. No. 1.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 201;
                                                                                                                                                                                                                                                                                            to sequence presented AF008561"
                                                                                                                                                                                                                                                                                                                                                                                   6
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                                                                                                                                                                                                                                                                                                                                  4254. .4259
/gene="G7c"
                                                                                                                                                                                                                                                                                                                                                                              1310 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 52.4
Matches 225; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1540 ACTGAAGAC 1548
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ORGANISM
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HQDLTEEAALNVTLVLFLEQPHPGRPRLHVEDYRGRTLLADDIFAAYFGPGFSSRRFR
AAGGEVSRANAAQDFLAFKSNPDLHFDAERLVQGRTRLVGALRETLVAARALEYTLA
RQRLGAALHALQDPYSRSNNVFLGERPQPHPLLMPRQELMSLAQVGDPTCSDCEGLSC
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Scock, M., Albertella, M.R., van Kooij, M., Wixon, J., van Vugt, H., de Groot, K. and Campbell, R.D.
Groot, K. and Gampbell, R.D.
G7C, a novel gene in the mouse and human major histocompatibility complex class III region, possibly controlling lung tumor
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Submitted (12-MAR-1999) Molecular Genetics, the Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands
1. 4312
/organism="Mus musculus"
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region that is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                          AF134319 4312 bp mRNA ROD 11-MAY-2000
Mus musculus G7c protein (G7c) mRNA, G7c-d allele, complete cds.
AF134319
261 GCCTTGGGGGGTGGAGAAGCCTGAGATGTGCCTGTCAGCCCTGCAGCTGGCCTGCTG 320
                                                                  gttgccaacccggctccttcatctacgtcttctcggatgcccgtgccaaggactaccac 542
                                                                                            543 aagaagaatgagctcctgcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctg
                                                                                                                                                                                  Snoek, M., Van Kooij, A., van Vugt, H. and de Groot, K.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Snock, M., Teuscher, C. and van Vugt, H.
Molecular analysis of the major MHC recombinational located within the G7c gene of the murine class III involved in disease susceptibility
J. Immunol. 160 (1), 266-272 (1998)
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/chromosome="17"
/map="19.00 cM; between G7a and G7"
/tissue_type="brain"
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Immunogenetics 51 (4-5), 383-386 (2000)
20260998
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/protein_id="AAF61401.1"
/db_xref="G1:7381105"
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/gene="G7c"
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em: EMBL; Sw.: SMISSPROT; Tr.; TREMBL; Wp.: WORMPEP: Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGPC/bhrl
GS1-164L12 is from the library Genome_Systems_ReleaseI VECTOR: pBeloBAC11
This sequence is the entire insert of clone GS1-164L12 The true left end of clone GS1-15303 is at 103097 in this sequence.
Submitted (18-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequestEsanger.ac.uk
On May 4, 2000 this sequence version replaced gi:7634143.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequence map criteria sollows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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13006. .13612
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10808. .11111
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12089. .12200
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/note="MIR repeat: matches 23. .152 of consensus"
6902. .7098
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7006="7 copies 4 mer ttat 96% conserved"

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/clone="GS1-164L12"
1. .798
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/note="LIME2 repeat: matches 5602.
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/note="AluSq repeat: matches 1.
9440. .9901
/note="MLTID repeat: matches 1.
10595. .10771
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12255. .12361
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/note="match: GSS: Em:AQ761942"
2792. .3250
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'note="match: GSS: Em:AQ246643"
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/db_xref="taxon:9606"
/chromosome="1"
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/note="14 cop
3435. .3488
/note="27 cop
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138/9. .13981 138/9. .14392 100te="LiM2 repeat: matches 2048. .2147 of consensus" 13982. .14292 /note="Aluva5 repeat: matches 1. .311 of consensus" 14293. .15642 /note="LiM2 repeat: matches 640. .2048 of consensus" 15608. .15818 /note="LiPa15-16 repeat: matches 146. .337 of consensus" /note="LiPa2 repeat: matches -752. .-208 of consensus" 16704. .16704 /note="LiM2 repeat: matches -676. .-428 of consensus" 16497. .1702 1721. .19291 /note="Li repeat: matches 1051. .2708 of consensus" 19471. .19528 ure complement(21071. 21467)

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John (22863)

Joh consensus /note="L1MEc repeat: matches 1211. .1677 of consensus" of consensus" .5793 of consensus" 7.00ce-18 Copies 2 mer tg 97% conserved" 26952. 26987 7.00ce-19 copies 4 mer tgtg 97% conserved" 27687. 27917 7.00ce-19 Libuo repeat: matches 83. .304 of consensus" 29345. 29476 /note="LIM1 repeat: matches 5180. .5793 of consensus 1364. .13877 /note="Aluso repeat: matches 27. .287 of consensus" 13879. .13981 consensus .2696 of consensus" .2690 of consensus" consensus. consensus .307 of consensus" .256 of consensus" /note="match: STS: Em:G37800"
38212. .38679
/note="LiMul repeat: matches 5847. .6324 of conse 40470. .40593
/note="MIR repeat: matches 8. .140 of consensus"
41014. .41123 .141 of consensus" .299 of .2750 of .297 of /note="Alusx repeat: matches 14. 32321. 32866 /note="match: GSS: Em:AQ418559" 33201. 33334 /note="AluSq repeat: matches 18. complement(37223. .37713) /note="L2 repeat: matches 2562. 33363. 33795 //note="L2 repeat: matches 2250. 35271. 35548 /note="AluY repeat: matches 39.
13683. .44142 /note="L2 repeat: matches 2605. 30393. .30828 /note="match: GSS: Em:AQ667379" 37319. .37339 /note="match: GSS: Em:AQ825928" 30990. .31275 matches 20. matches 10. /note="MIR repeat: m 41395. .41618 /note="MIR repeat: m 43230. .43494

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clone GS1-118G19 on chromosome 1q25.1-31.1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 125752 TCACTGTGTGTTTGAGTGGGCCTTCTCCCAATGATTGAAATTCGCAATCCTTTAGGTGAGA 125811
                     45533 . 45571

/note="AluJb repeat: matches 3. .41 of consensus"

45604. .46929

700te="L1PA7 repeat: matches 4758. .6124 of consensus"

46930. .47199

/note="AluJb repeat: matches 24. .297 of consensus"

47358. .47823
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54340. .54856
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              repeat: matches 2530.
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complete sequence.
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ALECT SUBMISSION SANGER CENTRE, Hinkton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On May 17, 2001 this sequence version replaced gi:13990347.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with only a small overlapping clone, as we submit sequences with any a small overlapping clone, as we submit sequences with this sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats: all regions were covered by at least one plasmid subclone or more than one Mil subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: EMBL; Sw., SWISSPROT; Tr., TREMBL; Well and the feature cannot be found a attention on the WORMPEP there.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MPORTANT: This sequence is not the entire insert of clone GS1-118G19 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone GS1-164112 is at 87362 in this sequence. The true right end of clone GS1-204112 is at 100 in this sequence. Location/Qualifiers
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5634. .5814
/note="MIR repeat: matches 59. .247 of consensus"
complement(5905. .5949)
/note="Sequence confirmed by AC023275 sequenced by WUGSC"
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hote="LIMA9 repeat: matches 5177. 5779 of consensus"
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/note="IJMA9 repeat: matches 4500. .5146 of consensus" 3794. .3891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.sanger.ac.uk/HGb/Chr1
GS1.118G19 is from the library Genome_Systems_ReleaseI VECTOR:
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/note="AluJo repeat: matches 19. .297 of consensus" 1618. .2109
/note="LIMA9 repeat: matches 5783. .6270 of consensus" 110. .2157
2110. .2157
2110. .2256
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/note="L2 repeat: matches 2572. .2706 of consensus"
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/clone_11b="Genome_Systems_Release1"
5. :571
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/organ1sm="Homo sapiens"
/db_xref="taxon:9606"
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7074. .7136
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1 13926. 13962 /note="Charlie3 repeat: matches 878. .914 of consensus" 13963. 17229 /note="LimbB repeat: matches 5745. .6173 of consensus" 42231. .42396
/note="LimbA repeat: matches 5483. .5646 of consensus" 42531. .42960
/note="LipbA repeat: matches 5721. .6157 of consensus" 43280. .44137
/note="Liz repeat: matches 1880. .2750 of consensus" /note="Liz repeat: matches 1880. .2750 of consensus" 10408 .10856 .rrun. matches D. .459 of consensus" /note="MLTIC repeat: matches 2. .466 of consensus" 10884 .11020 /note="MLT2B repeat: matches 210. .363 of consensus" 11056 .13925 /note="Librar repeat: matches 13. .2882 of consensus" 13926 .13962 repeat: matches 50. .112 of consensus" repeat_region misc_feature misc_feature misc_feature

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/note="Alusx repeat: matches 1. .296 of consensus"
51693 .51718
/note="13 copies 2 mer tt 100% conserved"
52326 .5250
/note="MIR repeat: matches 76 .244 of consensus"
52558 .5269
/note="MIR repeat: matches 75 .149 of consensus"
52640 .52807
/note="MIR repeat: matches 75 .149 of consensus"
53640 .52807
/note="L2 repeat: matches 1729 .2035 of consensus"
53456 .53885
/note="L2 repeat: matches 2285 .2730 of consensus"
54156 .54481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54316. .54481
/note="83 copies 2 mer tt 56% conserved"
55019. .55530. .55530. .55530. .55531. matches 1211. .1474 of consensus"
56353. .56911
/note="LiM4 repeat: matches 3491. .4067 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 tgatgcaggtgatcgacggcgcctcacgcattctggagcgcagtctgagcagccgcagcc 315
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                                                                                                                                                                                                                                                                                                                               /note="12" repeat: matches 1235. .1662 of consensus" 49871. .49964
/note="MIR repeat: matches 20. .127 of consensus" 49991. .50252
/000e="MIR repeat: matches 173. .456 of consensus" 50253. .50564
                                                                                                                                                                                                                                                                                            /note="L2 repeat: matches 2027. .2233 of consensus"
49480. .49851
                                                                                                                                                                            .2750 of consensus"
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                                                     note="AluSx repeat: matches 5. .311 of consensus"
14684. .44934
                                                                                                                                                                                                                   /note="Alux repeat: matches 1. .310 of consensus"
48164. .48425
                    note="MSTD repeat: matches 1. .134 of consensus"
4374. .44680
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                                                                                                                                  note="L2 repeat: matches 1247. .1880 of 6831. .46872
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63.3%; Pred. No. 0.0001;
tive 0; Mismatches 62;
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/note="L2 repeat: matches 2709.
47636. .47950
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18443. .48632
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Matches 107; Conservative
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AC023275 180248 bp DNA PRI 09-MAY-2001 Homo sapiens BAC clone RPI1-375L10 from 1, complete sequence. AC032275.3 GI:9838169

Homo sapiens

HTG. human.

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AC023275/c LOCUS DEFINITION

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Mapping Information for this clone was provided by Dr. John D.
Mapping Information of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (17-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
5 (bases 1 to 180248)
Waterston, R.H.
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Submitted (08-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
7 (bases 1 to 180248)
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                                                                                                                                                                                                                                                                3 (bases 1 to 180248)
Materston R.H.
Direct Submission
Submitted (10-FEB-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 180248)
Sulston,J.E. and Waterston,R.
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                                                                                                                                                                                                                Swearengen, S., Maupin, R., Drone, K. and Gregory, S. The sequence of Homo sapiens BAC clone RP11-375L10 Unpublished
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Web site: http://genome.wustl.edu/gsc
Contact: saplens@watson.wustl.edu
Center project name: H_NH0375L10
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                                                                                                            Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
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The RPCI-11 human BAC library was made from the blood of one male donor, as described by Oscegawa, K., Woon, P. Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome

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Research Genetics, Inc. (http://www.resgen.com) or Pleter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3: NEOURNCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-375L10; actual and is at base position 180248 of RP11-375L10.
Location/Qualifiers
1. 180248
                                                                                                                                                                                                                                                                                                                                                                                                                                    /rpt_family="L2"
8956. 9011
7.pt_family="MER1_type"
9685. 9725
7.pt_family="L1"
                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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7344. .17461
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(8161. .18263
                                                                                                                                                                                                             /clone="RP11-375L10"
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24419. .24688
/rpt_family="Alu"
24689. .26014
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6767.7258
/rpt_family-"L2"
7348.7653
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12790. .12957
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22832. .23003
/rpt_family="L1"
23004. .23307
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23308. .23700
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2246. .12330
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/rpt_family="CR1"
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/rpt_family="MIR"
5140. .5262
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7848. .8645
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(6593. .17278
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23740. .24219
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26047. .26106
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6076. .6593
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 356)
Weissenbach,J.

Direct Submission
Submitted (Ol-SEP-1955) Genethon, B.P. 60, 91002 Evry Cedex France.

E-mail: Jean.Weissenbach@genethon.fr

(bases 1 to 356)
Dib,C., Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A., Millasseau,P., Marc,S., Hazan,J., Seboun,E., Lathrop,M., Gyapay,G., Morissette,J. and Weissenbach,J.

A comprehensive genetic map of the human genome based on 5,264
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251502.1 G1:1232802
STS; CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA;
microsatellite marker; repeat polymorphism.
                                                      1 (bases 1 to 717)

Hunt, S., Sinas, S., Willey, D., Carter, N. and Ross, M.

Direct Submission
Submitted (07-MAR-2000) E-mail contact; humquery@sanger.ac.uk
Marker sts668667; (Primer A : CCTCCTGARATGGGACC;

Primer B : TGGAYGTTARATCGTGCTCG; amplimer size : 121 bp) was
developed from a single pass sequencing read from H.sapiens
Illow-sorted chromosome 9-12 random shear fragment, SC9-12pJ34g10.
Vector : pUC18 site : Smal
Purther information : http://www.sanger.ac.uk/HGP/Chr9/.
                Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 717)
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/clone_lib="SC9-12pJ"
198 c 211 g 120 t 2 othe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.3%; Score 65.4; DB 11; 72.4%; Pred. No. 0.0028; tive 0; Mismatches 32;
                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
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/chromosome="1"
/cell_line="CEPH 134702"
/clone_lib="genomic DNA"
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96176476
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Location/Qualifiers
1. .356
                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                 /sex="male
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Best Local Similarity 72.4%
The conservative 84; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             EST W86641 (NID:91400389) zh63e05.s1"
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STS from H.sapiens random shear fragment, sequence tagged site.
AL159308.1 GI:7210622
STS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               196 ccacaggagacgccaccctggccttcgtcttcgatgtcaccggctccatgtgggacgatc 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 6.8%; Score 69.8; DB 9; Length 180248; Best Local Similarity 63.3%; Pred. No. 8.3e-05; Matches 107; Conservative 0; Mismatches 62; Indels 0;
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33434. 33836
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34177. 34516
7note="similar to E
35831. 35967
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/rpt_family="Alu"
36643, 36920
/rpt_family="CRI"
36969, 37038
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37823, 38255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /rpt_family="Alu"
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/rpt_family="Alu"
46948. .47236
/rpt_family="Alu"
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39802. 39869
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                                                                                      27044. .27199
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                  26433. .26642
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27044. .27199
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repeat_region

repeat_region repeat_region repeat_region

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misc_feature misc_feature

repeat_region

repeat_region repeat_region repeat_region

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RESULT 14 HSJ34G10/c DEFINITION ACCESSION VERSION KEYWORDS SOURCE

LOCUS

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/note="cloning vector is M13mp18" 79 c 46 g 107 t 13 others
             BASE COUNT
ORIGIN
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	ó;
	Gaps
356;	ö
Length	Indels
11;	36;
Score 61.6; DB 11; Pred. No. 0.02;	0; Mismatches
6.0%;	vative
Similarity); Conser
Query Match Best Local Similarity 68.7%;	Matches 7

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ò g Search completed: March 7, 2002, 20:44:19 Job time: 6992 sec

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1031
1 tctagcgaaccccttcggcc.....agcccggctcgagcggccgc 1031
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                        11351937 seqs, 5372889281 residues
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Maximum Match 100%
Listing first 45 summaries
                                                      OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result Ouery No. Score Match Length DB ID C 1 309 30.0 470 10 A1449932 C 2 90.4 77.4 7.5 937 13 CRS025DE 4 70.6 6.8 559 11 BF418902 C 5 64 6.2 915 13 A2187837 C 7 55 5.3 754 13 A2189426 C 7 55 5.3 754 13 A2189426 C 8 49.6 4.8 935 13 CNS0091P C 11 46.4 4.5 925 13 CNS0091P C 12 46.4 4.5 925 13 CNS0091P	RIES			Description	2 AI449932 mr81b03.x	7	AL181931 7	BF418902	7 AZ137837 SP_0178_A	BE508854	AZ189426	AL066051	AL053013		AL053013	7
Score Match Length DB 309 30.0 47.4 7.5 937 13 77.4 7.5 937 13 77.4 7.5 937 13 61 5.9 528 10 55 5.3 754 13 48.8 4.7 925 13 46.6 4.5 520 11 46.6 4.5 952 13 46.6 4.5 925 13 46.6 4.5 925 13 46.6 4.5 925 13	SUMMA			ID	AI44993	A298507	CNS025D	BF41890	AZ13783	BE50885	AZ18942	CNS006X	CNS0091	BG89516	CNS0091	CNS022L5
S. S				DB	10	13	13	11	13	10	13	13	13	11	13	13
S. S				Length	470	720	937	559	915	528	754	935	925	520	925	965
ω : :		æ	Query	Match	30.0	8.8	7.5	6.8	6.2	5.9	5.3	4.8	4.7	4.5	4.5	4.5
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16	4	•	392	11	BF481089			
17	4.	•	406	11	BG560698			2
18	ω.	•	523	1	BG240204			OV1_19_B
19	ω.	•	924	13	SR		AL305554 T	Tetraodo
c 20	ς.	•	543	10	AW124542		AW124542 U	I-M-BH2
21	2		461	10	AU174537		AU174537 A	AU174537
22	*	•	632	11	BG744240		BG744240 6	0272334
c 23	7	٠	503	10	AI653725		AI653725 w	,b36f06.
24	٦.	•	989	11	BG835990		BG835990 Z	.m06_06h
c 25	41.4	4.0	384	10	AA294693		AA294693 S	WOV 3 MCP
56	ij	4.0	476	10	BE477180		BE477180 1	.60761 E
7	Ξ.	4.0	266	10	AW082912		AW082912 x	xc04c11.x
c 28	Η.	4.0	872	11	BG345072		BG345072 H	IVSME900
58	4	•	647	11	BG180123		BG180123 6	0232970
e	41	4.0	778	10	AI991270		AI991270 W	wu41h01.x
m	41	4.0	814	10	AW081400		AW081400 x	:c41h07.
c 32	0	4.0	523	10	AI855212		AI855212 6	03010C
m	o.	4.0	256	11	BG874151		BG874151 M	MEST46-H0
٣	ö	•	564	13	AQ848793			LMAJFV1_]
m	40.8	4.0	286	10	BE553066		BE553066 9	46088HC
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m	ö	•	979	10	AI855245		AI855245 6	03010H1
38	o.	4.0	671	13	AQ901789		A0901789 L	LMAJFV1_
39	0	•	813	11	BG321263		BG321263 Z	Zm04_03g0
4	·	•	926	13	CNS03GMI		AL243171 T	etraodo
c 41	٥.	•	460	10	A1432376			tg54h07.
4	0	•	573	10	BE452815			1066
4	40.6	3.9	738	11	BG864336			27
44	0	•	459	10	AW504911		04911	-HF-
45	o.	•	470	11	BF313055		22	9681
					ALIGNMENTS			
RESULT	1							
A1449952/C		00000	,	١	VNO#	9		0

RESULT 1 A1449932/c LOCUS DEFINITION	AI449932 470 bp mRNA EST 09-MAR-1999 mr81b03.x1 Stratagene mouse heart (#937316) Mus musculus CDNA clone IMAGE:603821 3' similar to WP:F1SG9.4 CE01552 IG SUPERFAMILY
ACCESSION VERSION KEYWORDS SOURCE	REPEATS;, mRNA sequence. A1449932 A1449932.1 GI:4293462 EST. house mouse.
ORGANISM REFERENCE	mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus. 1 (bases 1 to 470)
AUTHORS	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
TITLE JOURNAL COMMENT	Macelscon, R. and Missol, A. The WashU-NCI Mouse EST Project 1999 Unpublished (1999) Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
FEATURES	This clone was previously sequenced on the 5' end only, this new data is from the 3' end Possible reversed clone: polyT not found High quality sequence stop: 467. Location/Qualifiers 1470

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Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 720)

Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

ISlam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly

'M., Rose,M., Rose,M., Stokes,R., Tingey,A., von Niederhausern,A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2M0266L17R Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0266L17 R, DNA sequence.
                                                                         79 gcagcctccggctcagcatgacgcctagggcgcagctcctgccgctgctcctggcgacct 138
                                                                                                                                                                                                                                                                                                                                                                         139 acacagtagtggcggcgggcggtcacatctgatgagcccacgaagacgctgtcccccgcca 198
                                                                                                                                                                                                                                                                                                                                                                                                                                 tgcaggtgatcgacggcgcctcacgcattctggagcgcagtctgagcagccgcagccgg 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 TGCAGGTGATCGACGCCCTCGCGCATTCTGGAGCGCAGCCTGAGCAGCCGCAGCCGGG
                                                                                                                                                                                                                                                                                   ö
                       /db_xref="taxon:10090"
/clone="IMAGE:603821"
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                                                                                                                                                                                                                                                   30.0%; Score 309; DB 10; Length 470; 92.8%; Pred. No. 2.9e-57; .1ve 0; Mismatches 25; Indels
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
            /strain-"NIH/Swiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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AZ985073/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114 (gilAF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coll X110-Gold (Stratagene) cells and selected for ampliallin resistance."
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                                                                                                                                                                                                                                                                                                                                                                                                          /lab_host="E. coli strain XL10-Gold, Tl-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        937 bp DNA GSS 12-MAY-2000 nigroviridis genome survey sequence PUC-Ori end of clone library G from Tetraodon nigroviridis, genomic survey
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1 (bases 1 to 937)
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                                                                                                                                                                                                                                                                                                                                                          /clone_lib="Mouse 10kb plasmid UUGC2M library"
/sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8.8%; Score 90.4; DB 13; Length 720; 72.0%; Pred. No. 8.9e-10; tive 0; Mismatches 46; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: ddunnegenetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0266 row: L column: 17
                                                                                                    Plate: 0266 row: L column: 17
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                    Class: plasmid ends
High quality sequence stop: 720.
Location/Qualifiers
1. 720
                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="UUGC2M0266L17"
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GSS; genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis
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Matches 118; Conservative
Tel: 801 585 5606
Fax: 801 585 7177
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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                                                                                                                                                                                              Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and deissenbach, J. Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 559)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                    2 (bases 1 to 937)
Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF418902 559 bp. mRNA EST 28-NOV-2000 UI-R-BJ2-bgk-c-06-0-UI.S1 UI-R-BJ2 Rattus norvegicus cDNA clone UI-R-BJ2-bgk-c-06-0-UI 3', mRNA sequence. BF418902 GI:11406891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             453 CCATCCCGGAGGCGCATCGACGCTGGCGTTCGTCTTCGACGTGACCGCCTCCATGTACGA 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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/note="Genoscope sequence ID : C0AG236CG05SP1-end :
                                                                                                                                                                                                                                                                                                                Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
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/db_xref="taxon:99883"
/clone="236N09"
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Pred. No. 5.9e-07;
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Best Local Similarity 66.5%;
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285 c
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BF418902
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Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.ulowa.edu
Oligo-dT track not found, Not I site shown in beginning of sequence
01igo-dT track not found. Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Colne distribution: clones will be available through
Research Genetics (www.resgen.com) The following repetitive
elements were found in this cDNA sequence: 227-278, >(GAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_1U_R-BJ2'bqk-c-06-0-UI"
/clone_lib="UI-R-BJ2"
/lab_hok="DH108 (Life Technologies)" with a modified
/note="Vector: pT7130-pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ2
library is a subtracted library derived from the following
lissues: heart, atrium at 15 dpc, ventricle at 16.5 dpc,
atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
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Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray,
G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and
Hood, L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously described in (Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SEQ=None found"
137 c 152 g 127 t
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Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euceninoidea; Echinosea; Echinoidea;
Strongylocentrotidea; Strongylocentrotus.
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Pred. No. 1.8e-05;
0; Mismatches 64;
                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"/strain="Sprague-Dawley"/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                          Seq primer: M13 Forward
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Best Local Similarity 63.0
Matches 109; Conservative
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AZ137837/c
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Gaps

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Length 528;

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/d_xref="taxon:835"
/d_xref="taxon:835"
/clone="IMAGE:3397021"
/clone="IMAGE:3397021"
/clone="IMAGE:3397021"
/lab_host="bH10B (phage-resistant)"
/note="Organ: llver; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
AVerage insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC)
library."
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Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Blondi,T.R.,
Swartzell,S., Wallace,J.C., Poustka,A.J., Livingston,B.T., Wray
,G.A., Ettensohn,C.A., Lehrach,H., Britten,R.J, Davidson,E.H. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                    198 acaggagacgccaccctggccttcgtcttcgatgtcaccggctccatgtgggacgatctg 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 ACAGTGACTTCATCTCTGACTTTTCTGGTGGACACCACTGGTTCCATGGCGGATGACCTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             258 atgcaggtgatcgacggcgtctcacgcattctggagcgcagtctgagcagccgcagccgg 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 CAACAGTTGAAGGAGGCCTACACCTGGTTACTTAGCAGCGTTTCTGTTCAGTTCCCATGT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              424 GACTGCCCAGAATATGCAATGGGTGGACTTAAGTTGCTTTGCAGGAATCACCCCATAAT 483
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoldea; Euchinoldea; Echinocea; Echinolda;
Strongylocentrotidae; Strongylocentrotus.
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Pred. No. 0.0022;
0; Mismatches 175; Indels
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California Institute of Technology
Pasadena California 91125, USA
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Fax: (626) 793-3047
Email: acameron@caltech.edu
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Best Local Similarity 48.7%;
Matches 166; Conservative
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AZ189426/C
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Other_ESTS: dclabfor.x1

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-rémail.nih.gov
Tissue Produrement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DA Sequencing by: Washington University Genome Sequencing Contextioned distribution: Kanopus clones from this library are available through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

High quality sequence stop: 430.

Location/Qualifiers

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1.528
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/db_xref="taxon:7668"
/clone="Plate=178 Col=20 Row=1"
/clone=lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli DH108"
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Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia: Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus
1 (bases 1 to 528)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
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                                 Hood,
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Best Local Similarity 62.5%; Pred. No. 0.00048;
Matches 100; Conservative 0; Mismatches 60
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                        Contact: Cameron, RA, Davidson, EH, Division of Biology 156-29
California Institute of Technology Pasadena California 91125, USA
                                                                                                               Tel: (626) 395-8421
Fax: (626) 799-3047
Email: accomeronicaltech.edu
Plate: 178 row: I column: 20
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 915.
Location/Qualiflers
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423

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/clone_lib="RPCI-98"
/clone="BACR14N09"
/note="end : T7"
                                                                                                                                                                                                    Matches 122; Conservative
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazuctoy Ososogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoxI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://www.individual.edu/drosophila_bac.htm.
                                                                                                                                                                          /clone="Plate=1014 Col=11 Row=A"
Clone="Plate=1014 Col=11 Row=A"
Clone=10P="StrongyJocentrotus purpuratus, purple sea
urchin, sperm genomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACRI4N09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ALO66051 GI:4945019
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 935)
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                                                                                                                               /organism="Strongylocentrotus purpuratus'
/db_xref="taxon:7668"
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/db_xref="taxon:7227"
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP prosophila melanogaster BAC library was prepared by Razutoyo Oscogawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 925)
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                                                                                                                         Length 935;
                                                                                                                      4.8%; Score 49.6; DB 13; 29.0%; Pred. No. 0.64;
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Casas, E.,
           þe
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Fabrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                              filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
_Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         540 KCGSTTBGSTTTTTTSSGSGYGKGCSSGSBSCSCCSSCSSSSSSCSCCBCCCCSSSY 599
                                                                                                                                                                                                                                                                                                                                                                            65 gtcccattagggctgcagcctccggctcagcatgacgcctagggcgcagctcctgccgct 124
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                                                                                                                                                                                                                                         Length 925;
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358378 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG895162
EG895162.1 GI:14305403
                                                                                                                                                                    511 others
                                                                           melanogaster"
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PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4399
                                                                                                                                                                                                                                         DB 13;
                                                                                                                                                                                                                                   Query Match 4.7%; Score 48.8; DB Best Local Similarity 15.5%; Pred. No. 0.96; Matches 60; Conservative 167; Mismatches
                                                                                                                                                                172 t
                                                                    /organism="Drosophila m
/db_xref="taxon:727"
/clone=llb="RPCI-98"
/clone="BACRI9D16"
/note="end : TPT3"
a 61 c 61 g 1
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Litect Aubmissor.

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr |
- Web: www.genoscope.cns.fr |
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruifiy.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or
                                                                                                                                                                                                                                                                                                         /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108 gegeagetectgeegetgetectggegacetacacagtagtggeggeggeggteacatet 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210 GTCGACTTCAACAAGGCCAAGTCCCCGCTACCAGGAGATGCCACAAGAGCACATAGGCTGC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 gatgagcccacgaagacgctgtccccgccacaggagacgccaccctggccttcgtcttc 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gatgicaccggciccatgigggacgatcigatgcaggigatcgacggcgccicacgcatt 287
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0; Mismatches 104; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                                                                                    1. .520
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC_IPIG"
/tissue_type="pooled"
/lab_host="DH10B"
PCR PRIMEIS
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
Plate: 121 row: M column: 3
Seg primer: ATTTAGGGGACACTATAG.
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51.2%;
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AL178322.1 GI:7816379
GSS; genome survey sequence.
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopteryqii; Neopteryqii; Teleostei; Buteleostei; Neoteleostei;
Actinopteryqii; Neopteryqii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
1 (bases 1 to 965)
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cost.crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 using
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Tetraodon nigroviridis genome survey sequence T7 end of clone
227L10 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                805
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                                                                                                                                                                                                                                                                                                         ceteceggeteageatgaegectagggegeagetectgeegetgetectggegaectacae 142
                                                                                                                                                                                                                                                                                                                              ggtgatcgacggcgcctcacgcattctggagcgcagtctgagcagccgcagccggggtcat 322
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                                                                                                                                                                                                                                                                      Gaps
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Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agtagtggcggcggtcacatctgatgagcccacgaagacgctgtcccccgccacgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    203 agacgccacctggccttcgtcttcgatgtcaccggctccatgtgggacgatctgatgca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   744 SAGSVVSSASSSSSSSSSSSSSSVSCSSVASSMSCSSBSSSSASASSSSSSSSSSSSSSCASCCCT
filters for hybridization from the BACPAC Resource Center found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
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                                                                                                                                                               511 others
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                                                                          melanogaster"
                                                                                                                                                                                                                                  Query Match 4.5%; Score 46.4; DB 13;
Best Local Similarity 12.7%; Pred. No. 3.2;
Matches 38; Conservative 142; Mismatches 120;
                                                                                                                                                               172 t
                                                                     /organism="Drosophila mv/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR19D16"
/note="end : TET3"
a 61 c 61 g 1'
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Submitted (12-APF-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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GSS: genome survey sequence.
Tetraodon nigroviridis.
Tetraodon nigroviridis.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei, Buteleostei; Neoteleostei;
Actinopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae, Tetraodon
1 (bases 1 to 818)
Roest-Crollius; H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C.,
Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Welssenbach, J.
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                                                                                                                                                                                                                                      /note="Genoscope sequence ID : C0AG227DF05LP1-end : T7" 268\ c 296\ g 186\ t 1\ others
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Tetraodon nigroviridis genome survey sequence T7 end of clone
008E16 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggccatcaaggctgccgtggaggttgccaaccccggctccttcatctacgtcttctcgga 520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 GICCCCCAAGCIGGCCITAGCCAACGCICCCACCAATICCGAGAIGTICCTCTICACGGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              521 tgcccgtgccaaggactaccacaagaagaatgagctcctgcagctcctgcagctgaagca 580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 965,
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genome. For more information, please take a http://www.genoscope.cns.fr/Tetraodon. Location/Qualifiers
                                                                                       1. .965
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="227110"
/clone_lib="G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                                                                                                                                                                                                                                           DB 13;
                                                                                                                                                                                                                                                                                                                                                                                     Score 46; DB 13
Pred. No. 3.9;
0; Mismatches
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Best Local Similarity 54.2%;
Matches 116; Conservative
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Genoscope.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
Clade; Panicoideae, Andropogoneae; Sorghum.
1 (bases 1 to 375)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
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                                                                                ID : COBG008BC08LP1~end : T7" t 178 others
                                                                                                                                                                                                                                              187 tgtccccgccacaggagacgccacctggccttcgtcttcgatgtcaccggctccatgt 246
                                                                                                                                                                                                                                                                      gccgcagccgggtcatcgccaactatgcgctggtgcctttccacgacccagacattggcc 366 : :: :: |:| :: |: | ::
                                                                                                                                                                                                                                                                                                                                                                                                                                             443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 422 tgttcagggaggtggtgactgcccagaaatgagtgtgggggccatcaaggctgccgtgga 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                       247 gggacgatctgatgcaggtgatcgacggcgcctcacgcattctggagcgcagtctgagca
                                                                                                                                                                                                                                                                                                                                                                                                                                  502 ISTSSSSBTTATTSASSTSSTSSBTSSTSTSSSSSTATSAASSTAASSASSTSATSS

        BF481079
        375 bp
        mRNA
        EST
        05-DEC-20

        FM1_16_B06.b1_A003 Floral-Induced Meristem 1 (FM1) Sorghum PorpLinguum cDNA, mRNA sequence.
        BF481079
        BF481079
        GI:11551900

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Contact: Cordonnier-Pratt MM
                                                                                                                                                                           DB 13; Length 818;
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/db_crofone="008E16"
/clone_lib="G"
/note="Genoscope sequence ID : COBG
104 c 245 g 149 t 178
                                                                                                                                                                     ch 4.4%; Score 45; DB 13; L Similarity 25.9%; Pred. No. 6.4; 87; Conservative 101; Mismatches 143;
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/db_xref="taxon:132711"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSSGCAGASGSSCTCTSACASSSCTSSSASSTSTC 287
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High quality sequence stop:
POLYA-No.
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/clone_lib="Floral-Induced Meristem 1 (FM1)"
//chote="Organ: Floral-Induced meristems; Vector:
pBluescript II from Lambda Zap II; Site_l: XhoI;
ECORI, mature plants were placed in a growth chamber for I5 days with 16 hr darkness and 8 hr light (flowering is induced by short-day conditions); I6 days after being returned to the greenhouse under natural long days during late April/early May, meristems were harvested The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG560654 379 bp mRNA EST 10-APR-2001
RHIZ2_58_B04.bl_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
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/db_xref="taxon:132711"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda
Zap II; Site_1: XhoI; Site_2: EcoRI; The library was made
from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Sorghum.
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The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       560 gcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctgactggggactgcggtga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 ccgcacccacctggctacctggcttttgaggagatcgcctccaccagttctggccaagt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 GACCTCGCCAAGGTCGACCTACGCGCTGACGTGCTCGGGGCAGTCAAATCCGATGACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 379)
Cordonnier-Pratt, M. M., Gingle, A., Paterson, A., Sudman, M.
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An EST database from Sorghum: Sorghum propinguum rhizomes
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                       Score 44.8; DB 11;
Pred. No. 7.3;
0; Mismatches 87;
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Contact: Cordonnier-Pratt MM
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BG560654.1 GI:13589652
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Seg primer: JEN REV
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Best Local Similarity 52.7%;
Matches 97; Conservative
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BASE COUNT 85 a 103 c 130 g 61 t
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Query Match 4.3%; Score 44.8; DB 11; Length 379;
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	Matches 9/; conservative U; Mismatches 0/; indets U; days U;	560 gcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctgactgggggactgcggtga 619	
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Db 114 GCAGCAGCACCTGGTGCTGGCGCACAGCTGTTCTTCTTCTGCGGCTCCGACGTCGA 173

Qy 620 ccgcaccctggctacctggcttttgaggagatcgctccaccagttctggccaagt 679

Qy 740 ggcc 743

Search completed: March 7, 2002, 21:07:19 Job time: 8057 sec

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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AI449932 mr81b03.x	AZ985073 2M0266L17	AL181931 Tetraodon	BF418902 UI-R-BJ2-		BE508854 dcl3h07.y	AZ189426 SP_1014_A	BG895162 358378 MA	AL066051 Drosophil	AL178322 Tetraodon	AL234371 Tetraodon	
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SUMMARIES	AI449932	AZ985073	CNS025DE	BF418902	AZ137837	BE508854	AZ189426	BG895162	CNS006XK	CNS022L5	CNS039U2	BF481079
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% Query Match Length DB	470	720	937	559	915	528	754	520	935	965	818	375
% Query Match	29.1	11.0	4.6	8.6	7.8	7.4	6.7	5.6	5.6	5.6	5.5	5.4
Score	240	90.4	77.4	9.07	64	61	52	46.6	46.2	46	45	44.8
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44 45			470	,	NMENTS		
RESULT 1 AI449932/C LOCUS		AI449932		2	MRNA		. 666
DEFINITION	_	Mr81b03.x1 IMAGE:60382 REPEATS;	1 Stratago 821 3' sin , mRNA se	agene mos similar sequence	use heart (#937 to WP:F15G9.4 C	316) Mus musculus cDNA e E01552 IG SUPERFAMILY	SDNA clone
VERSION VERSION KEYWORDS SOURCE ORGANISM	SW]	A1449932.1 EST. house mouse. Mus musculus	1 GI:429. se. lus	93462			
		Eukaryota Mammalia;	; Metazoa Eutheria	7. S	ordata; Craniata; V dentia; Sciurognath	Craniata; Vertebrata; Euteleostomi Sciurognathi; Muridae; Murinae; Mu	eostomi; nae; Mus.
REFERENCE AUTHORS	63.60	1 (bases Marra,M., Underwood ,B., Swal ,E., Kohn	1 to 470 Hillier, ,K., Step ler,T., G ,S., Shin ,R. and W) L., toe, ibbo ibbo 'T.,	Kucaba,T., Martin,J M., Theising,B., Al ns,M., Pape,D., Har Jackson,Y., Carden	Martin,J., Beck,C., Wylle,T ng,B., Allen,M., Bowers,Y., e,D., Harvey,N., Schurk,R., ., Cardenas,M., McCann,R.,	e,T., ., Person ., Ritter
TITLE JOURNAL COMMENT		The WashU Unpublish Contact: Washingto 4444 Fore	ed (1999) Marra M/W n Univers st Park P	e ES ashU ity arkw	The WashU-NCI Mouse EST Project 1999 Unpublished (1999) Contact: Marra M/WashU-NCI Mouse EST Proj Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Tel: 314 286 1800)ect 1999 couis, MO 63108,	USA
		Fax: 314 Email: mot This clone This Cons This clone data is fi Possible High cmal	314 286 1810 : mouseest@watson.wustl clone is available roya : Consortium (info@inage clone was previously se is from the 3' end ble reversed clone; pol ble reversed clone; pol	tson labl info viou ven clon	314 286 1810 : mouseest@watson.wustl.edu clone is available royalty-free throu ccosortium (info@inage.lnl.gov) for clone was previously sequenced on the is from the 3' end ble reversed clone: polym not found munality sequenced store store 467	gh LLNL ; cont further infor 5' end only,	act the mation. this new
FEATURES source	rce	1	Location/Qualifiers 1470	Qual	ifiers		

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SM Muss muscalus.

Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria: Rodentia; Sciurognathi; Muridae; Murinae. Mus.
E 1 (bases 1 to 720)

S Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvai, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)

Contact: Robert B. Weiss
University of Utah Genome Center
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2M0266L17R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0266L17 R, DNA sequence.
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                                                                                                                                         /tissue_type="heart"
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/dev_stage="13 day embryos"
/lab_host="sOLR (kanamycin resistant)"
/note="organ: heart; Vector: pBluescript SK-; Site_1:
BCORI; Site_2: XhoI; Cloned unidIrectionally. Primer:
Oligo dT. 93 pooled NIH/Swiss 13 day embryo hearts.
Average insert size: 1.0 kb; Uni-ZAP XR vector; -5'
adaptor sequence: 5' GAATTGGGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTTTTTTTTTTTTTTTTT"

a 152 c 168 g 69 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 geggteacatetgatgageeceaegaagaegetgteeecegeeacaggagaegeeaeetg 120
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/clone="IMAGE:603821"
/clone_lib="Stratagene mouse heart (#937316)"
/sex="pooled"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 29.1%; Score 240; DB 10; Length 470; Best Local Similarity 92.6%; Pred. No. 1.1e-44; Matches 252; Conservative 0; Mismatches 20; Indels
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84112, USA
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Insert Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69 cregreccrirccaceacccaegragaecccc 38
  musculus"
organism="Mus"
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared bNA was blunt end-repaired with T4 DNA polymerase and T4 polymcleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gal electrophoresis. Vector DNA was prepared from a derivative of pwMax (gilfa3214)gplAF129072.1), a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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                                                                                                                                                                            /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UGGZM0266L17"
/clone=lib="Wouse 10kb plasmid UUGCZM library"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 236N09 of library G from Tetraodon nigroviridis, genomic survey
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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetraodontidae; Tetraodon.

1 (bases 1 to 937)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bulneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
Charaterization and repeat analysis of the compact genome of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        331 cagggaggtggtgactgcccagaaatgagtgtgggggccatcaaggctgccgtggaggtt 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 CAGGGAGGTGGTGTCCAGAAATGAGCATCGGGGCTATAAAGATTGCCTTGGAAATC 215
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Pred. No. 1.3e-10;
0; Mismatches 46;
Plate: 0266 row: L column: 17
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 720.
Location/Qualiflers
                                                                                                                                                            /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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AL181931.1 GI:7820017
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72.0%;
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Matches 118; Conservative
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Best Local &
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TITLE

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/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/dlone_lib="UI-R-BJ2 bgk-c-06-0-UI"
/clone_lib="UI-R-BJ2"
/lab_host="NetCor: pT773D-Pac (Pharmacia) with a modified
/note="wetCor: pT773D-Pac (Pharmacia) with a modified
polylinker; Site_l: Not I; Site_2: ECO RI; The UI-R-BJ2
polylinker; Site_l: Not I; Site_2: ECO RI; The UI-R-BJ2
plylinker; Site_l: Not I; Site_2: ECO RI; The UI-R-BJ2
plylinker; Site_l: Not I; Site_2: ECO RI; The UI-R-BJ2
plylinker; Site_l: Not I; Site_2: ECO RI; The UI-R-BJ2
plylinker; Site_l: Not I; Site_2: ECO RI; The UI-R-BJ2
plylinker; Site_1: For J derived from the following
tissues: heart, atrium at 15 dpc, ventricle at 15 dpc,
atrium at 16.5 dpc, ventricle at 13 dpc, ventricle at 15
dpc, AV canal at 15 dpc. For a detailed description of
the library from which this clone was derived, please
visit our web site at ratest-eng.ulowa.edu. The
subtraction has been previously described in (Bonaldo,
Lennon and Soares, Genome Research 6:791-806, 1996)
TAG_SED=None_lend"
177
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Eukaryota: Metazoa: Echinodermata; Eleutherozoa; Echinozoa;
Echinodea; Euchinodea; Echinodea;
Echinostae; Echinodea; Echinodea;
Strongylocentrotidae; Strongylocentrotus.

1 (bases 1 to 915)
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R.,
Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray,
G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and
Hood, L.
is likely internal to the message. cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) The following repetitive elements were found in this cDNA sequence: 227-278, >(GAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AZ137837 915 bp DNA GSS 28-AUG-2000 SP_0178_A2_E10_SP6E Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate=178 Col=20 Row=1, DNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A sea urchin genome project: Sequence scan, virtual map, and additional resources
Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            226 ategecaactatgegetggtgeettteeacgaeceagaeattggeecagtgae 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 70.6; DB 11;
Pred. No. 3.8e-06;

    .559
    /organism="Rattus norvegicus"

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California Institute of Technology
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Az137837.1 GI:8289740
GSS.
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Seq primer: M13 Forward
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ilarity 63.0%;
Conservative
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Matches 109; Conserv
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Fax: 319 335 9565
Exai: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Ollgo-dT track not found, Not I site shown in beginning of sequence
                                                                                                                                                                                                                                                                       Direct Submission
Submission
Submitted (12-ARP-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                 Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                            2 (bases 1 to 937)
coest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 559)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/db_xref="taxon:99883"
/clone="11b="G"
/clone_11b="G"
/note="Genoscope sequence ID : COAG236CG05SP1-end
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Program for Rat Gene Discovery and Mapping
University of Iowa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 77.4; DB 13;
Pred. No. 1.2e-07;
0; Mismatches 56;
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Rattus norvegicus
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Length 559; Indels

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Best Local Simi
Matches 166;
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ORIGIN
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AZ189426/C
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Amphibita; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 528)
1 (bases 1 to 528)
1 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
I Unpublished (1997)
1 Other_ESTs: dc13h07.xl
Contact: Robert Strausberg, Ph.D.
Contact: Robert
                                                                                                                                                                                                                                                                       /organism="Strongylocentrotus purpuratus"
//db.xref="taxon;7668"
//clone="Plate="18 Col=20 Row=I"
//clone_lib="Strongylocentrotus purpuratus, purple sea
//clone_lib="Strongylocentrotus purpuratus, purple sea
//nchln, sperm genomic BAC library"
//note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE508854 528 bp mRNA EST 07-AUG-2000 dcl3h07.yl NICHD XGC Lil Xenopus laevis cDNA clone IMAGE:3397021 5/similar to WP:F15G9.4A CE18595 ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 acaggagacgccaccctggccttcgtcttcgatgtcaccggctccatgtgggacgatctg 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 ACTGGCGGAACAACGATGGCTTTTTTTTTTTAACGGGATCCATGTTTGATGACTTG 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 atgcaggtgatcgacggcgtctcacgcattctggagcgcagtctgagcagccgcagccgg 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 64; DB 13;
Pred. No. 0.00013;
0; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 t
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/db_xref="taxon:8355"
/clone="IMAGE:3397021"
/clone_lib="NICHD XGC Li1"
Pasadena California 91125, USA Tel: (626) 395-8421 Fax: (626) 793-3047 Email: acameron@caltech.edu Plate: 178 row: I column: 20 Seq primer: SP6 Class: BAC ends High quality sequence stop: 915. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                               174 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BE508854.1 GI:9728629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 African clawed frog.
Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                            219 c
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AUTHORS
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BE508854
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SOURCE
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/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pCWV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 1.4 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection (XGC)
) library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AZ189426 754 bp DNA GSS 30-AUG-2000 SP_1014_AI_AG_SPGE Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic chone Plate=1014 Col=11 Row=A, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                             103 acaggagacgccacctggccttcgtcttcgatgtcaccggctccatgtgggacgatctg 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     184 ACAGTGACTTCATCTCTGACTTTTCTGGTGGACCCACTGGTTCCATGGCGGATGACCTT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 atgcaggtgatcgacggcctcacgcattctggagcgcagtctgagcagccgcagccgg 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      283 acggcggacccagtggtgtttcagagagagctgagacaactctatgttcagggaggtggt 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                343 gactgcccagaaatgagtgtgggggccatcaaggctgccgtggaggttgccaacccggc 402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          424 GACTGCCCAGAATATGCAATGGGTGGACTTAAGTTGGCTTTGCAGGAATCACCCCATAAT 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             map, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 244 CAACAGTTGAAGGAGGCCTACACCTGGTTACTTAGCAGCGTTTCTGTTCAGTTCCCATGT
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Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)
20402566
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                                                                                                                                                                                                                                                                                                                          Length 528;
                                                                                                                                                                                                                                                                                                                7.4%; Score 61; DB 10; Length 52 ilarity 48.7%; Pred. No. 0.00057; Conservative 0; Mismatches 175; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 tectteatetaegtetteteggatgeeegtgeeaaggaeta 443
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California Institute of Technology
Pasadena California 91125, USA
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Seg primer: SP6
Class: BAC ends
High quality sequence stop: 754.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ÃZ189426
AZ189426.1 GI:8372518
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Fax: (626) 793-3047
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DB 11;

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Score 46.6; DB
Pred. No. 1.1;
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                                                 Query Match 5.6%;
Best Local Similarity 51.2%;
Matches 109; Conservative
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Matches 112; Conserv
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CNSO06XK/C
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VERSION
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TITLE
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Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 520)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
                                  /organism="Strongylocentrotus purpuratus"
/db_xref="taxon:7668"
/clone="plate=1014 Col=11 Row=A"
/clone_lib="Strongylocentrotus purpuratus, purple sea
urchin, sperm apenomic BAC library"
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli
                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine (not believed (2000))
Contact: Smith TPL USDA, ARS, US Meat Animal Research Center
DO BOX 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: pCMV SPORT6; Site_1: Xbal, Site_2: Xhol; Library made from pooled tissue from day 11, 13, 15, 20
                                                                                                                                                                                                                                                                                                               103 acaggagacgccaccctggccttcgtcttcgatgtcaccggctccatgtgggacgatctg 162
                                                                                                                                                                                                                                                                                                                                                                                      163 atgraggtgatcgacgcctcacgcattctggagcgcagtctgagcagcagccgcagccgg 222
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                                                                                                                                                                                                                                                                                                                                                                                                                   303 CACCAGGGTATTGAAGGAGCAGAACGGAATTTGGAATTTGGAGAGGAGAACAAG 244
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                                                                                                                                                                                                                                      Score 55; DB 13; Length 754; Pred. No. 0.014;
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358378 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence.
BG895162
                                                                                                                                                                                                                                                                             70; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 GCCTTGGAAAAACTTGCCTTGGGGGCCCTTTCAAGGTTCAGGGTTGGG 197
                                                                                                                                                                   211 t
                                                                                                                                                                                                                                                                               0; Mismatches
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/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BACKWARD: GTTTTCCCAGTCACGACG
Plate: 121 row: M column: 3
Seq primer: ATTTAGGTGACACTATAG.
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Location/Qualifiers
1. .754
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Best Local Similarity 58.1%;
Matches 97; Conservative
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Direct Submission

B pl 191006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web 192 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucyoo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by Partial Econt digestion of Drosophila DNA provided by the BDGP from the Isogenic strain y2; cn bw 4p, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or fillters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14N09 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                73 gatgageceaegaagaegetgteeeegeeaeagaagaegeeaeeetggeettegtette 132
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Bukaryota; Meoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                         13 gegeageteetgeegetgeteetggegaeetacacagtagtggeggeggeggteacatet 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-JUN-1999
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   0; Mismatches 104; Indels
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29.4%; Pred. No. 1.5;
tive 90; Mismatches 178;
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Direct Submission
Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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1 (bases 1 to 965)

Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Charaterization and repeat analysis of the compact genome of the
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                                 885 CSCSSSSCCCSSCSCGCSCGCSCGGSSCCSCGCGSSSSGCGCCCSGGSCGCCCGSCG 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO22L5 965 bp DNA GSS 12-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone
227L10 of library G from Tetraodon nigroviridis, genomic survey
                                                                        65 teacatetgatgageceaegaagaegetgteeceegeeaeggagaegeeaeetggeet 124
                                                                                                              825 GSCSCCSSSCCGCGCGCGCGCGCGGCSGGCGSSGCGGCSGGCGGSSCCGCSG 766
                                                                                                                                                     125 tegtettegatgteaceggetecatgtgggaegatetgatgeaggtgategaeggeget 184
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cgcctagggcgcagctcctgccgctgctctggcgacctacacagtagtggcggcggcgg
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cost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fishe
Bernot, A., Flzames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
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/organism="Tetraodon nigroviridis"
/ba.rref="taxon:99883"
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/clone_lib="G"
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Tetraodon nigroviridis.
Tetraodon nigroviridis
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This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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1 (bases 1 to 818)

2 (bases 1 to 818)

Boots-Crothius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Weissenbach, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
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         : COAG227DF05LP1~end : T7"
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Tetraodon nigroviridis genome survey sequence T7 end of clone
008E16 of library G from Tetraodon nigroviridis, genomic survey
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/clone_llb="G"
/note="Genoscope sequence ID : COBGOO8BCO8LP1~end : T7"
/ note="Genoscope sequence ID : COBGOO8BCO8LP1~end : T7"
                                                                                                                                                                                                   366 ggccatcaaggctgccgtggaggttgccaaccccggctccttcatctacgtcttctcgga 425
                                                                                                                                                                                                                                              225 GICCCCCAAGCIGGCCITAGCCAACCCICCACAATICCGAGAIGITCCICITCACGGA 166
                                                                                                                                                                                                                                                                                           426 tgcccgtgccaaggactaccacaagaagaatgagctcctgcagctcctgcagctgaagca 485
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                                                                                                                                                                                                                                                                                                                                                                                   486 gtcgcaggtggtcttcgtgctgactggggactggcggtgaccgcaccctggctacct
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boost-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fish
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W. and Weissenbach, J.
                                                                                                                       Length 965;
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/clone="008E16"
                                                                                                                    DB 13;
       tΒ
                                                                                                                Score 46; DB 1
Pred. No. 1.7;
0; Mismatches
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       sequence
g 186
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Tetraodon nigroviridis.
Tetraodon nigroviridis
/note="Genoscope
268 c 296
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Best Local Similarity 54.2%;
Matches 116; Conservative
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Gaps

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//organism="Sorghum propinguum"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/db_xref="taxon:132711"
/clone_lib="Rhizomes" (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda 2ap II; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda 2AP II.
Clones to be sequenced were prepared by mass excision."
a 103 c 130 g 61 t
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RHIZ2_58_B04.bl_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
1 (bases 1 to 379)
Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Prat
poly-A RNA in the cloning vector to be sequenced were prepared by
                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2000)
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1805
Fax: 706 542 1805
                                                                                                                                                                                                                   465 gcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctgactggggactgcggtga 524
                                                                                                                                                                                                                                        ,L.H.
An EST database from Sorghum: Sorghum propinguum rhizomes
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                                                                                                                                    Length 375;
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Pred. No. 2.6;
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                                                                                                                                      Score 44.8; DB 11;
Pred. No. 2.6;
                                                                                                                                                                                87;
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                                                              63 t
                                                                                                                                                                                  0; Mismatches
    library was made from |
lambda ZAP II. Clones |
mass excision."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@uga.edu
Seg primer: JEN REV
High quality sequence stop:
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG560654.1 GI:13589652
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Best Local Similarity 52.7%;
Matches 97; Conservative (
                                                                                                                                        / Match 5.4%;
Local Similarity 52.7%;
les 97; Conservative 0
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Best Local S
Matches 97
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//organism="Sorghum propinguum"
//db xref="taxon:132711"
//clone_lib="Floral-Induced Meristem: 1 (FM1)"
//clone_lib="Floral-Induced meristems: Vector:
pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:
ECORI: mature plants were placed in a growth chamber for
ECORI with 16 hr darkness and 8 hr light (llowering is
induced by short-day conditions); 16 days after being
returned to the greenhouse under natural long days during
late April/early May, meristems were harvested The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 375)
Cordonnier-Pratt, M.-M., Gingle, A., Sudman, M., Marsala, C. and Pratt
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An EST database from Sorghum: floral-induced meristems Unpublished (2000) - Contact: Cordonnier-Pratt MM Contact: Cordonnier-Pratt MM Department of Botany The University of Georgia Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA The: 706 542 1860 Fax: 706 542 1805
                                                                                                                                                                                                                                                                                                                                                                                                                              327 tgitcagggaggtggtgactgcccagaaatgagtgtgggggccatcaaggctgccgtgga 386
                                                                                                                                                                                                                                                                                              272 cagigaccotcacggcggacccagiggigiticagagaga----gcigagacaacicia 326
                                                                                                                                                                                                                                                                                                                                                                             tgtccccgccacaggagacgccacctggccttcgtcttcgatgtcaccggctccatgt 151
                                                                                                                                    152 gggacgatctgatgcaggtgatcgacgcctcacgcattctggagcgcagtctgagca 211
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FWI_16_B06.bl_A003 Floral-Induced Meristem 1 (FM1) Sorghum
propinguum cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                         212 gccgcagccgggtcatcgccaactatgcgctggtgcctttccacgacccagacattggcc
                                                                        5;
                                   Length 818;
                                                                          Indels
                                   5.5%; Score 45; DB 13; L
ilarity 25.9%; Pred. No. 2.7;
Conservative 101; Mismatches 143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ggttgccaaccccggctccttcatctacgtcttctc 422
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High quality sequence stop: 342
POLYA=No.
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                                                            Similarity
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                                         Query Match
Best Local
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BF481079
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Sudman, M. and Pratt

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BG560698
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/db.xref="taxon:132711"
/clone_lib="Filoral-induced Meristem 1 (FM1)"
/clone_lib="Filoral-induced Meristem; Vector:
/clone_lib="Filoral-induced Meristem; Vector:
/note="Organ: Floral-induced in a growth chamber for
/noted by short-day conditions); 16 days after for
/noted by short-day conditions); 16 days after being
/returned to the greenhouse under natural long days during
/noted paraly May, meristems were harvested The
/library was made from poly-A RNA in the cloning vector
/noted names excision."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Cordonnier-Pratt MM
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
slade, Panitoideae, Andropogoneae, Sorghum.
(Dases 1 to 392)
Cordonnier-Pratt, M., Gingle, A., Sudman, M., Marsala, C. and Pratt
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                                114 GCAGCAGCCGCACCTGGTGCTGGCGCACAAGCTGTTCCTTCTGTCGCGCTCCGACGTCGA 173
                                                                                                                                            465 gcagctcctgcagctgáagcagtcgcaggtggtcttcgtgctgactggggactgcggtga 524
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 gcagctcctgcagctgaagcagtcgcaggtggtctcgtgctgactggggactgcggtga
                                                                    525 ccgcacccaccctggctacctggcttttgaggagatcgcctccaccagttctggccaagt
                                                                                                                                                                                                                                                                                                                            BF481089 392 bp mRNA EST 05-DEC-20
FML_16_C06.bl_A003 Floral-Induced Meristem 1 (FM1) Sorghum
BF481089
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Pred. No. 2.6;
0; Mismatches
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High quality sequence stop: 350
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BG550698 406 bp mRNA EST 10-APR-2001
RHIZ2_S8_F04.bl_A003 Rhizome2 (RHIZ2) Sorghum propinguum cDNA, mRNA
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Cordonnier-Pratt,M.-M., Gingle,A., Paterson,A., Sudman,M. and Pratt
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/organism="Sorghum propinguum"
/orb_xef="taxon:132711"
/clone_lb="Rhizomes" (RHIZ2)"
/note="Organ: Rhizomes; Vector: pBluescript II from Lambda Zap II; Site_l: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II.
clones to be sequenced were prepared by mass excision."
a 101 c 151 g 64 t
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Sorghum propinguum
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Sorghum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     / An EST database from Sorghum: Sorghum propinguum rhizomes
Uppublished (2000)
Contact: Cordonnier-Pratt MM
Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1860
Fax: 706 542 1860
Sea primer: JEN REV
High quality sequence stop: 386
POLYA-NO.
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ccgcacccacctggctacctggcttttgaggagatcgcctccaccagttctggccaagt
                           465 gcagctcctgcagctgaagcagtcgcaggtggtctcttcgtgctgactggggactgcggtga
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5.4%; Score 44.8; DB 11;
Best Local Similarity 52.7%; Pred. No. 2.6;
Matches 97; Conservative 0; Mismatches 87;
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BG560698.1 GI:13589696
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1111 Db 239 GGC 242 Search completed: March 7, 2002, 21:07:21 Job time: 8059 sec

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US-09-665-728-1
1403
1 MTPRAQLLPLLLATYTVVAA.....IEVRDPLGMSQGSPPLLMQD 275
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/SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
/SIDS2/gcgdata/geneseqf/geneseqp/AA1982.DAT:*
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/SIDS2/gcgdata/geneseg/genesegp/AA1990.
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                           522463 seqs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                      OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp/AA2000.DAT:*

/SIDS2/gcgdata/geneseq/geneseqp/AA2001.DAT:*

		•	Description	Rat secreted factor	Sections at /332818	Murine SHD1 protei	TODATO COURT	Sovbean magnesium	S. equisimilia atre	Trincated Met atre	Amino acid segment	Amino acid sequence	Amino acid appropri	Amino acid sequenc
SUMMARIES				7		m	4	2	2	2	9		4	5
SUMM			ID	AAB8314	AAY5366	AAB98973	AAB8612	AAB4825	AAR2020	AAR1289	AAY8400	AAY84007	AAY84004	AAY84005
			DB	22	21	22	22	22	13	13	21	21	21	21
			Match Length DB ID	275	3117	353	1017	750	414	369	372	384	401	413
	dР	Query	Match	100.0	44.8	8.3	7.0	9.9	9.9	6.5	6.5	6.5	6.5	6.5
			Score	1403	628.5	116	96	93	92.5	91.5	91.5	91.5	91.5	91.5
		Result	No.		7	n	4	S	9	7	ω	6	10	11

27-SEP-2000; 2000WO-US26582.

WO200123419-A2

05-APR-2001

99US-0156277.

27-SEP-1999;

e (SK repto pptoki e. S eavab	Met-core streptoki Met-core streptoki OmpAL streptokinas Porcine phosphoino Porcine G-protein Pig pl20 regulator A mouse transgluta Corn magnesium che	SE LOCKOLLIN	sp. fotei form form vaul pro se (1 stre
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112 114 116 118 119	2011001 201001 201001	, 8 9 0 0 1 2 E 4 7 7 7 7	2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4

Rat; secreted factor; P00210D09; cardiant; nephrotropic; antiinflammatory; gene therapy; cardiac disease; renal disease; inflammatory disease. Rat secreted factor encoded by clone P00210D09. 35..55 /label= Transmembrane_domain 123..143 /label= Transmembrane_domain 1..21 /label= Signal_peptide 22..275 /note= "Rat secreted factor" Location/Qualifiers AAB83147 standard; protein; 275 AA. (first entry) 29-JUN-2001 Rattus sp. AAB83147; Key Peptide Protein Domain Domain AAB83147 RESULT

ALIGNMENTS

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14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 126;
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ID AAB9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mechanical stress; gene therapy; protein 608; osteoporosis; bone density; bone development; g1/3328186.
                                                                               Novel secreted factor encoded by clone P00210D09 useful for diagnosing, treating and/or preventing various cardiac, renal and inflammatory
                                                                                                                                               The present sequence is a novel secreted factor encoded by rat cDNA clone P00210D09. The invention relates to a polypeptide comprising a sequence of at least 80% identity to residues 22.122 of the present sequence, or a sequence encoded by a nucleic acid hybridising under stringent conditions to the complement of the coding region comprising 1031 nucleotides, and having at least one biological activity of the polypeptide encoded by clone P00210D09. The polypeptides and polynucleotides of the invention are useful for the treatment of cardiac, renal and inflammatory diseases. The polynucleotides are useful in antisense mediated gene inhibition and in gene therapy. The polypeptides are useful in assays for identifying lead compounds that may be used as therapeutic agents in the treatment of cardiac,
                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGDCPEMS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                        VGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPG 180
                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                              YLAFEEIASTSSGQVFQLDKQQVSEVLKWVESAIQASKVHLLSADHEEEGEHTWRIPFDP
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                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 1403; DB 22; Length 275; 100.0%; Pred. No. 2.2e-138; 1.1ve 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence gi/3328186 from an alignment with protein 608.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 slkevtislsgpgpeievrdplgmsggsppllmgd 275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY53667 standard; Protein; 3117 AA
                                                                                                                                                                                                                                                                                           or inflammatory diseases.
                                                                                                                             Claim 9; Fig 1; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-FEB-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.
Matches 275; Conservative
                        Stanton LW, Kapoun AM;
                                             WPI; 2001-328177/34.
                                                                                                                                                                                                                                                                                                                275 AA;
(SCIO-) SCIOS INC.
                                                         N-PSDB; AAF82464
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The present sequence is obtained from a clustral X alignment with protein 608. Protein 608 was identified using the method of the invention after subjecting rate osteoblasts to mechanical stress. Expression of the cost of genes was found to be upregulated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the identification of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue or cells comprising bone cells), isolating the specific cellular fractions and extracting mRNA from them, and differentially analysing the mRNA in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identified genes are employed in determining risk associated with a physiological or disease state. The risk determination methods are used for testing a medicament for gene this responsive to a specific stress. The invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or the symptoms or other factors causing or contributing to osteoporosis or its symptoms or other conditions involved in mechanical stress or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ж
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 SSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVE
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                                                                                                                                                                                                                                                                                                    determining risk and
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48.6%; Pred. No. 9.5e-56;
tive 51; Mismatches 69;
                                                                                                                                                                                                                                                                                                    Identification of stress induced genes for detern preventing, treating or controlling osteoporosis
                                                                                                                                                                                Feinstein E,
                                                                                                                                                                                                                                                                                                                                                                                               Claim 32; Fig 6A-R; 308pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB98973 standard; protein; 353 AA.
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                                                        98US-0085673
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                                                                                                                       (QUAR-) QUARK BIOTECH INC.
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                                                           15-MAY-1998;
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Best Local Similarity
                                                                                                                                            N-PSDB; AAF88175
                                                   25-OCT-1999;
                                                                             (BADI ) BASF
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03-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                  SHD1 protein useful for controlling the differentiation and activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant; formylglycinamidine-ribotide synthase; E.C. 6.3.5.3; herbicide; purine biosynthesis; defoliant; desiccant; transgenic.
                                                                                                                                                                                                                                                                                                                  The present invention relates to the murine SHDI protein shown here. I protein can be used for controlling differentiation and activation of germ centre B cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  :| :| |: :|| :|: |:|
114 lqgvddadaatvleaalatllavvar-----vrpeetrgaadpvllqtqvqegfg 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    105 -LRQLYVQGGGDCP------EMSVGAIKAAVEVANPGSFIYVFSDARAK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 pppsllrpppvllatvrylageva----grgdvscaevasfvadrlravrldls 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 slrrcyargkgpyprqaafqglfllynlgsleapaggstaalracpplgaalavdaafre 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYHKK-NELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIA-----STSSGQVFQLD 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               224 dnharlfrllrtlpylqs-----cavqehigyarrkalarlsralstpkgqtlpld 274
                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRAQLL---PLLLATYTVVAAAVTSDEPTKTLSPATGDATLA----FVFDVTGSMWDDL-
                                                                                                                                                                                                                                                                                                                                                                                                                                    82;
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                                                                                                                                                                                                                                                                                                                                                                                                             Length 353;
                                                                                                                                                                                                                                                                                                                                                                                                                                     98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | :: | :: | |: | 275 fiehflaldglqeardlcqahgltldkdrvvflrgqyseeg 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 KQQVSEVLKWVESAIQASKVHLLSAD------HEEEG 230
                           Mouse; SHD1; differentiation; germ centre B cell.
                                                                                                                                                                                                                                                                                                                                                                                                           Score 116; DB 22;
Pred. No. 0.0015;
                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB86124 standard; Protein; 1017 AA.
                                                                                                                                                                                                                                                                                          Claim 1; Page 6-7; 16pp; Japanese.
                                                                                                                                                                                   SUME ) SUMITOMO ELECTRIC IND
                                                                                                                                                                                                                                                                                                                                                                                                           8.3%;
                                                                                                                                 99JP-0263688
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                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.38
Best Local Similarity 24.99
Matches 70; Conservative
                                                                                                                                                                                                                                                               germ center B cells
                                                                                                                                                                                                            WPI; 2001-313371/33.
N-PSDB; AAH25841.
 Murine SHD1 protein.
                                                                                                                                                                                                                                                                                                                                                                       353 AA;
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                                                                             JP2001078778-A.
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                                                                                                       27-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel polynucleotide sequences from Arabidopsis thaliana, tobacco (Nicotiana tabacum) and Chilopsis linearis which contain the coding region for a plant formylglycinamidine-ribotide synthase (E.C. 6.3.5.3), an enzyme used in purine biosynthesis. The products of the invention have herbicide, defoliant and desicant formylglycinamidine-ribotide synthase can be expressed in prokaryotic or eukaryotic cells, e.g. to produce transgenic plants with increased resistance to herbicides that target formylglycinamidine-ribotide synthase and to prepare a test system for identifying inhibitors of formylglycinamidine-ribotide synthase. Such inhibitors are potentially useful as defoliants, desiccants or especially this sequence represents the tobacco formylglycinamidine-ribotide synthase. Such this sequence represents the tobacco formylglycinamidine-ribotide synthase. Such this sequence represents the tobacco formylglycinamidine-ribotide synthase described in the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50 MWDDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLY 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652 vleklcs----gavsaniiggvtsspivelrvdgvthlndktsvlrdm-weetsfglek 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 LLLATYTVVAAAVTSDEPTKTLSP--------ATGDATLAFVFDVTGS 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110 VQGGGDCPEMSVGAIKAAVEVANPGSF1--YVFSDARAKDYHKKNELLQLLQLKQSQVVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLTGDCGDRTHPGYLAFEEIASTSSGQVFQL------DKQQVSEVLKWVESAIQASK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Soybean magnesium chelatase subunit (clone sdp4c.pk022.h18[FIS]).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                                                                                                                                                                  New DNA encoding formylglycinamidine-ribotide synthase of plantuseful for identifying enzyme inhibitors, potential herbicides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22; Length 1017;
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                                                                                                                                                                                                                      Kunze G;
                                                                                                                                                                                                                  Boldt R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.0%; Score 98; DB 19.9%; Pred. No. 0.56 Live 52; Mismatches
                                                                                                                                                                                                              Sonnewald U,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 2; Page 54-58; 60pp; German.
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                                                                    99DE-1051443.
17-OCT-2000; 2000WO-EP10204
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                                                                                                                                                                                                                  Lerchl J, Ehrhardt T,
                                                                                                                                                                                                                                                                                       WPI; 2001-316337/33.
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Matches
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                                                                                                                                                                                                                                                                                                 The invention relates to nucleic acid fragments encoding magnesium chelatase subunits. The nucleic acid fragments may be used to create transgenic plants in which the new polypeptides are present a thigher or lower levels than normally found, and for overexpression in bacterial or yeast hosts to efficiently produce large amounts of the encoded or yeast hosts to efficiently produce large amounts of the encoded or yeast hosts to efficiently produce large amounts of the encoded or polypeptides which could then be used for screening different compounds for potential herbicidal activity. The polynucleotides may also be used as probes for genetic and physical mapping the genes that they are part of, and as markers for traits linked to these genes. Such information is useful in plant breeding. The polypeptides are used for preparing antibodies, which are useful for detecting the polypeptides in situ or in vitro, and as a target to facilitate design and/or identification of inhibitors of enzymes that may be used as herbicides. Host cells may also be used directly for screening different compounds for potential culturity. The present sequence represents the soybean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                         Isolated nucleic acid fragments encoding magnesium chelatase subunits, useful as probes for genetic and physical mapping of genes, as markers for traits linked to these genes, and in plant breeding -
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647 ivaltdgranislkrstdpevaaatdapkpsaqelkdeilevagkiykagmsllvidten 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Indels 58; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PFHDPDIGPVTL--TADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVEVANPGS----F 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 VFVLTGDCGDRTHPGYLAFEEIASTSSGQVFQLDKQQ---VSEVLKWVESAIQAS 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 750;
                                                                                                                                                                   Maxwell CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 1.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%; Score 93;
                                                                                                                                                                  Gutteridge S,
                                                                                                                                                                                                                                                                          Claim 10; Page 60-62; 103pp; English.
                                                                                                                                     DUPO ) DU PONT DE NEMOURS & CO E I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                   02-JUN-2000; 2000WO-US15351
                                                                                                              99US-0137461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           magnesium chelatase subunit
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Matches 54; Conservative
                                                                                                                                                                 Famodu 00,
                                                                                                                                                                                       WPI; 2001-091215/10.
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                                                                                                                                                                                                      N-PSDB; AAC84571
                                  WO200075340-A2.
                                                                                                             04-JUN-1999;
           Glycine max.
                                                            14-DEC-2000.
                                                                                                                                                               Butler KH,
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The SKC-2 gene was isolated from S.equisimilis type C by gene amplification from the synthetic primers SK1, SK2 and SK3 (see AAQ20666-8). The SKC-2 gene was inserted into yeast expression vector PPS-7 for extracellular expression of streptokinase and into pNAO for intracellular expression in yeast. For expression in bacteria, the SKC-2 gene was inserted in plasmid pEKG3, between a trp promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 ddyfevidfas---datitdrn----gkvyfadkd-gsvtlptgpv-----qeffls 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 GG---GDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ---SQV 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 ghvrvrpykekpigngaksvdveytvgftplnpdddfrpglkdtkliktlaigdtitsge 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 DÖLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQ 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marrero LFH;
i, Somavilla MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Stroptokinase C-2 gene from S.equisimilis type C - plasmids and transformants for large scale intra- and extracellular expression of SKC-2 useful in thrombolytic agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 VFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASKVHLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 414;
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                                                      plasminogen activator; coronary thrombosis; ATCC-9542.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hidalgo AP, Doce RS, Mar
Munoz EAM, Martinez WB,
Martinez LSH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 6.6%; Score 92.5; DB 13;
Similarity 25.5%; Pred. No. 0.54;
56; Conservative 33; Mismatches 90;
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S.equisimilis streptokinase.
                                                                                                                                                                                                                                                                         91AU-0078101.
                                                                                                                                                                                                                                                                                                                               90CU-0000090.
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                                                                                                            Streptococcus equisimilis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Chaplen RR,
Ramirez AC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  García J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1992-024716/04.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fernandez AP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 ADHEE----
                                                                                                                                                                                                                                                                         31-MAY-1991;
                                                                                                                                                                                                                                                                                                                               23-MAY-1990;
                                                                                                                                                            AU9178101-A.
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De La Fuente Garcia JDJ;

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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
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Best Local Similarity 25.33
Matches 57; Conservative
                                                                                                                                                                                                                             Streptococcus equisimilis.
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Seralena Menendez A;
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N-PSDB; AAZ99251.
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The gene was truncated by 15 codons at the 3' terminal and engineered to add a Met codon prior to codon 16 of the minal and engineered to add a Met seque expression Streptokinase CDS. The construct was used to prepare expression vector pGC606 for prodn. of the streptokinase core molecule. See also AAR12887-R12889, AAR12891-R12893, AAR128885 and AAR12522.
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             antithrombotic; thrombolysis; streptokinase; thrombin.
                                                                                            Streptococcus equisimilis ATCC 9542 or ATCC 10009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                             2.369
/label= core streptokinase
/note= "AAs 16-383"
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                                                                                                                                                                                    Location/Qualifiers
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89GB-0027722.
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Best Local Similarity
Matches 57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prophylaxis.
                                                                                                                                                                                                                                                                                                                                                                                                                 WO9109125-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dawson KM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY84006,
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                                                                                                                                                                                                                                      Protein
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10;

51; Gaps

Indels

86;

AAY84006 RESULT

XEXEXEX

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Length 372;

AAY84004;

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RESULT 11
AAY84005
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKC-2. Streptokinase forms a complex with plasmingen, activating its conversion to plasmin. The SKC-2 gene was modified to produce the mutant protein. The obtained mutants conserve their capacity for plasminogen activator complex formation, thus having reduced antigenicity. The mutants are derived from the 1-1119 gene fragment, and retain the thrombolytic activity of SKC-2 but, compared with the full length protein, are less antigenic and retain activity better in presence of antibodies that neutralize activity of the complete protein. The mutants are thrombolytic agents which are useful for treating myocardial infarction, pulmonary thromboembolism, surgical complications and other forms of thromboshi; thromboembolism, surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  present sequence represents a mutant protein of the streptokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 DDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPV------VFQR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 ELROLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           163 --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         194 itsqellaqaqsilnkthpgytiyerdssivthdndifrtilpmdqeftyhvknreqaye 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garcia Ojalvo A, De La Fuente Garcia JDJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                            Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;
plasminogen activator complex formation; thrombolytic;
myocardial infarction; pulmonary thromboembolism; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 384;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 VHLLSADHEE-------EGEHTWRIPFDPS-LKEVTI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
               Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.5%; Score 91.5; DB 25.3%; Pred. No. 0.61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Mismatches
                                                                                                                                                                                                                                                                                                        (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 24-25; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY84004 standard; Protein; 401 AA
                                                                                                                                                                                                                                        99EP-0202639
                                                                                                                                                                                                                                                                        98CU-0000119
                                                                                                                                    Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 25.33
Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                       forrens Madrazo IDC,
                                                                                                                                                                                                                                                                                                                                                           Seralena Menendez A;
                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-226041/20.
N-PSDB; AAZ99252.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-terminus
                                                                                                                                                                                                                                      13-AUG-1999;
                                                                                                                                                                                                                                                                      14-AUG-1998;
                                                                                                                                                                    EP985729-A2
                                                                                                                                                                                                    15-MAR-2000
                                                                                                                   Synthetic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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AAY84004
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Recombinant production of streptokinase mutants, useful as thrombolytic agents for treating myocardial infarction, that are truncated at the N-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52 DDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPV------VFQR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163 --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132 pykekpiqnga-----ksvdveytvqftplnpdddfrpglkdtkllktlaigdt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 ELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ-
                                                                                                                                                                                                                                                                                                                                                                                                       De La Fuente Garcia JDJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                51;
                                                                                                     Streptokinase; SKC-2; plasminogen; plasmin; antigenicity;
plasminogen activator complex formation; thrombolytic;
myocardial infarction; pulmonary thromboembolism; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219 VHLLSADHEE-------EGEHTWRIPFDPS-LKEVTI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 6.5%; Score 91.5; DB 21; Best Local Similarity 25.3%; Pred. No. 0.65; Matches 57; Conservative 31; Mismatches 86;
                                                                   Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                 (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
                                                                                                                                                                                                                                                                                                                                                                                                    Garcia Ojalvo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 18-20; 54pp; English.
                                                                                                                                                                                                                                                                                                99EP-0202639
                                                                                                                                                                                                                                                                                                                                 98CU-0000119
                                  (first entry)
                                                                                                                                                                                            Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                    Torrens Madrazo IDC,
                                                                                                                                                                                                                                                                                                                                                                                                                      Seralena Menendez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-226041/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-terminus
                                                                                                                                                                                                                                                                                              13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                 14-AUG-1998;
                                  03-JUL-2000
                                                                                                                                                                                                                           EP985729-A2
                                                                                                                                                                                                                                                              15-MAR-2000
                                                                                                                                                                        Synthetic.
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RESULT 12

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104 ELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 pykekpiqnga-----ksvdveytvqftplnpdddfrpglkdtkllktlaigdt 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51;
                                                                                                                                                                                                                                                                                                                                                                                                                    De La Fuente Garcia JDJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.5%; Score 91.5; DB 21; Length 413; 25.3%; Pred. No. 0.68;
Live 31; Mismatches 86; Indels 51
                                                                                                                               Streptokinase; SKC-2; plasminogen; plasmin; antigenicity; plasminogen activator complex formation; thrombolytic; myocardial infarction; pulmonary thromboembolism; thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VHLLSADHEE------EGEHTWRIPFDPS-LKEVTI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86;
                                                                                                Amino acid sequence of a mutant streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                  (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
                                                                                                                                                                                                                                                                                                                                                                                                                    Garcia Ojalvo A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 20-21; 54pp; English.
AAY84005 standard; Protein; 413 AA
                                                                                                                                                                                                                                                                                                                   99EP-0202639
                                                                                                                                                                                                                                                                                                                                                   98CU-0000119
                                                                (first entry)
                                                                                                                                                                                                                 Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 25.3
nes 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    Forrens Madrazo IDC,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Seralena Menendez A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-226041/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           413 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAZ99250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or C-terminus
                                                                                                                                                                                                                                                                                                                   13-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                   14-AUG-1998;
                                                                03-JUL-2000
                                                                                                                                                                                                                                                 EP985729-A2
                                                                                                                                                                                                                                                                                  15-MAR-2000
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                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                               AAY84005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of the SK protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 DDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPV-----VFQR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 ELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          145 pykekpiqnqa------ksvdveytvqftplnpdddfrpglkdtkllktlaigdt 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95 ddyfevidfas---datitdrn----gkvyfadkd-gsvtlptqpvqefllsghvrvr 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK
                                                                                                                                                        Non-immunogenic; epitope; T-cell; immunogenicity; immune system; immunogl bulin; therapeutic; streptokinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.5%; Score 91.5; DB 20;
25.3%; Pred. No. 0.68;
tive 31; Mismatches 86;
                                                                                                                      Streptokinase (SK) protein sequence.
              AAW86143 standard; Protein; 414 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 6; Fig 28; 77pp; English.
                                                                                                                                                                                                                                                                                                                                                 98GB-0007751.
97GB-0010480.
97GB-0016197.
97GB-0025270.
97US-0067235.
                                                                                                                                                                                                                                                                                                                   98WO-GB01473
                                                                                                                                                                                                           Streptococcus equisimilis.
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Matches 57; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BIOV-) BIOVATION LTD
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31-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                       28-NOV-1997;
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                                                                                   03-MAR-1999
                                                                                                                                                                                                                                                                              26-NOV-1998.
                                                                                                                                                                                                                                                                                                                                                     14-APR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                AAW86143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr FJ;
AAW86143
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08-DEC-1999;
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                                                                                                                                                                                                                   AAB01295;
                                                                                                                                                                    AAB01295
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                                                                                                                                                                                                  The invention relates to a method for the production of non-immunogenic proteins. The method comprises determining at least part of the amino acid sequence of the protein; (b) identifying in the amino acid sequence one or more potential epitopes for T-cells (T-cell epitopes) of the given species; and (c) modifying the amino acid sequence to eliminate at least one of the T-cell epitopes identified in step (b) thereby to eliminate or reduce the immunogenicity of the protein when exposed to the immune system of the given species. A method of analysing a pre-existing protein to predict the basis for immunogenic responses is also provided. The methods can be used particularly for reducing the immunogenicity of immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The products can be used for diagnosis and therapy. The present sequence represents the amino acid sequence of a de-immunised SK protein molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10;
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95 ddyfevidfas---datitdrn-----gkvyfadkd-gsvtlptqpvqefllsghvrvr 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pykekpiqnga-----ksvdveytvqftplnpdddfrpglkdtkllktlaigdt 193
                                                                                                                                                                                                                                          Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK; immunogl bulin; therapeutic; streptokinase; de-immunised.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Reducing immunogenicity of proteins - by modifying the amino acid sequence of the protein to eliminate potential epitopes for T-cells of a given species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                   219 VHLLSADHEE-------EGEHTWRIPFDPS-LKEVTI
                                                                                                                                                                                                         De-immunised streptokinase (SK) protein sequence.
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                                                                                                             AAW86144 standard; Protein; 414 AA.
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97GB-0010480.
97GB-0016197.
97GB-0025270.
97US-0067235.
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                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                        Streptococcus equisimilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (BIOV-) BIOVATION LTD.
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28-NOV-1997;
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                                                                                                                                           AAW86144;
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Proteins or their fragments can be rendered non-immunogenic or less immunogenic by identifying one or more potential T cell epitopes and modifying the sequence to eliminate at less one of these T cell epitopes to reduce the immunogenicity of the protein when exposed to the immune system of another organism. The method can be used for the immune system of another organism. The method can be used for the immune system of another organism. The method can be used for the immune system of another organism, a vaccine, a protein used to convert inactive drugs to its active form within a living organism, a vaccine, a protein used as a carrier of other molecule or a protein which binds to other molecules within or introduced within the living organism in order to alter the bio distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicione, diagnosis and in manufacture of a therapeutic or a diagnostic agent. Streptockinase is produced by certain strains of beta-hemolytic streptockinase is protein has no inherent enzymatic activity but has considerable clinical importance of inherent enzymatic activity but has considerable clinical importance of inherent enzymatic activity but has considerable clinical importance of inscolution of fibrin filaments in blood clots. Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, improving survival and preserving left ventricular function following mycouring anthodies in humans generally limits the protein to a single use. The native protein is immunogenic and the protein to a single use. The native protein the sequence of the wild type streptokinase. The is altered streptokinase sequence
163 --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK 218
                                                                         Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug; vaccine; carrier; diagnosis; therapy; complement; C3; C5; CVF; plasminogen; streptokinase; fibrin; blood clot; thrombolysis; plasmin; myocardial infarction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wild type streptokinase from Streptococcus equisimilis.
                                                                                                                                                                                      21.9 VHLLSADHEE-------EGEHTWRIPFDPS-LKEVTI 247
                                                                                                                                                                                                                                                                Carter G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB01295 standard; protein; 414 AA.
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                                                                                                                                                                                                                              104 ELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ- 162
                                                                                                                                                                                                                                                                                                                                     194 itsqellaqaqsilnkthpgytiyerdssivthdndifrtilpmdqeftyhvknreqaye 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rendering a protein non-immunogenic or less immunogenic useful in medicine and in diagnostics involves determining the amino acid sequence of the protein, identifying and modifying potential epitopes
                                                                                                                                                           DDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPV------VFQR 103
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95 ddyfevidfas---datitdrn-----gkvyfadkd-gsvtlptgpvqefllsghvrvr 144
                                                                                                                                                                                                                                                                  145 pykekpignga-----ksvdveytvgftplnpdddfrpglkdtkllktlaigdt 193
                                                                                                                                                                                                                                                                                                     --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK 218
                                                                                                                             Gaps
                                                                                                                           51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenicity; immunogen; T cell epitope; T-lymphocyte; drug; vacche; carriter; diagnosis; therapy; complement; C3; C5; CVF; plasminogen; streptokinase; fibrin; blood clot; thrombolysis; plasmin; myocardial infarction.
                                                                                       6.5%; Score 91.5; DB 21; Length 414; 25.3%; Pred: No. 0.68; 11ve 31; Mismatches 86; Indels 51
is given in AAB01296. See GENESEQ records AAB01289-B01302
                                                                                                                                                                                                                                                                                                                                                                                                 219 VHLLSADHEE-------EGEHTWRIPFDPS-LKEVTI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Altered streptokinase from Streptococcus equisimilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carter G;
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                                                                                    Query Match
Best Local Similarity 25.34
Matches 57; Conservative
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                                     414 AA;
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                                     Sequence
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carrier of other molecule or a protein which binds to other molecules within or introduced within the living organism in order to alter the bod distribution of other molecules, such that the protein does not stimulate immune response in the living organism. The less immunogenic protein is useful in medicine, diagnosis and in manufacture of a therapeutic or a diagnostic agent. Streptokinase is produced by certain strains of beta-haemolytic streptococci. The protein has no inherent enzymatic activity but has considerable clinical importance owing to its ability to efficiently bind human plasminogen, potentiating its activation to plasmin and thereby promoting the owing to its ability to efficiently bind and thereby promoting the constitution of fibrin filaments in blood clots. Streptokinase is an effective thrombolytic agent in the treatment of coronary thrombosis, improving survival and presserving left ventricular function following production of neutralising antibodies in humans generally limits the production of neutralising antibodies in humans generally limits the protein to a single use. The new method could provide a longer therapeutic use for streptokinase. This is the sequence of the altered streptokinase. The wild type streptokinase sequence is given in AAB01295. See GENESED records AAB01289-B01302.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21; Length 414;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 AA;
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US-09-665-728-1 1403 1 MTPRAQLLPLLLATYTVVAA.....IEVRDPLGMSQGSPPLLMQD 275 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	Description	hypothetical	٤.	hypothetical prote		ď	hypothetical profe			-	P-qlycoprotein hom	major vault protei	receptor-like hist	receptor-like hist	hypothetical profe	amylopullulanase p	hypothetical prote	probable magnesium	integrin beta-3 su	beta-7	C	RAD23 protein homo	protein-qlutamine	protein disulfide-	streptokinase G nr	paraquat-inducible	lro protein - hima	platelet-derived a	probable ABC trans	P-glycoprotein-lik
SUMMARIES	QI .	T20992	T43290	T16199	T21560	150726	C84346	T27707	T16305	T14070	T48007	153908	T28655	T30898	T19941	A75207	A96771	T31461	151530	A46271	T27706	T04150	B45991	S32476	S02723	F82162	S57723	PFMSRB	F86155	D85023
	DB	7																		7	7	7	7	_	~	~	7	7	7	7
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di	Query Match	44.8	44.8	7.8	7.8	7.6	7.5	7.5	7.5								٠						6.5	٠.	•				6.3	6.3
	Score	628.5	628.5	110	109	106	105.5	105	105	101.5	96.5	96	93.5	93.5	93	93	92.5	92	92	91.5	91	90.5	90.5	89.5	œ	Ф.	88	88	88	88
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P-glycoprotein-lik probable ABC trans	probable fatty-aci	protoporphyrin IX	cellulose 1,4-beta	hypothetical prote	tenascin Y precurs	glycogen phosphory	secreted serine pr	streptokinase (EC	hydroxymethylaluta	hypothetical prote	M polyprotein prec
T52319 E86155	E69438 T45280	T02925	S47466	T30829	T42635 T06249	A42318	T36768	BZSO	S14955	T00330	GNVUBW
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30 31	33 33	3 4 5	36	37	3 6 8 6 8 6	40	41	42	43	44	45

ALIGNMENTS

RES	RESULT 1
TZ(1720992 Mypothetical protein F15G9.4a - Caenorhabditis elegans 7.Snerjas: Caenorhabditis algans
1(C) 1(C) 1/2 (C) 1/2	C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C.Accesion: T20992; T24733 R.Sulston. J
Sul A; F	submitted to the EMBL Data Library, December 1994 A Reference number: 219355
2 (A A	A:Status: preliminary; translated from GB/EMBL/DDBJ A:Nolecule type: DNA A:Nolecule type: DNA
A A A S. C. R. F. E. F. F. E. F. F. E. F. F.	A;Kesidues: 1-31/3 <w1l> A;Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a A:Experimental source: clone F15G9 R:Kershaw. J.</w1l>
Sul A; F	submitted to the EMBL Data Library, December 1994 A:Reference number: 219929
4 K	A/Status: preliminary; translated from GB/EMBL/DDBJ
2 E C	A; Molecule type: DNA A; Residues: 1-5175 <wiz-></wiz->
A C	avicuss references. Embilitation; FibnicAAA()344.1; GSPDB:GNUUUZ8; CESP:FIBG9.4a * Experimental source: clone T09B9 C.Generics:
Ø . A	A; Gene: CESP:F15G9.4a
A; I	ade position: A S/1; 320/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3;
	; 2312/2; 2353/3; 2659/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1
O m	Query Match Best Local Similarity 48.6%; Pred. No. 5.6e-45;
Σ	
QY	10 LLLATYTVVAAAVTSDEPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRILERSL 69
qa	15 LLLATTCSSVNDDKNDPTGKSSLAFVFDITGSMFDDLVQVREGAAKIFKTVM 66
Qy	70 SSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVE 129
qq	67 AQREKLIYNYIMVPFHDPYLGEIINTTDSTYFWRQLSKVYVHGGGDCPEKTLTGILKALQ 126
Qy	130 VANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIAS 189
qо	127 ISLPSSFIYVFTDARSKDYHLEDEVLNTIQEKQSSVVFVMTGDCGNRTHPGFRTYEKIAA 186
QY	190 TSSGQVFQLDKQQVSEVLKMVESAIQASKVHLLSADHEEEGEHTWRIPFDPSLKEVTISL 249
qa	187 ASFGQVFHLEKSDVSTVLEYVRHAVKQKKVHLMYEARERGGTVSRNIPVDKHLSELTISL 246

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Gaps 94

40;

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A; Description: The sequence of C. elegans cosmid F28B4.
A; Reference number: 218475
A; A; Accession: The sequence of C. elegans cosmid F28B4.
A; Accession: Th16199
A; Actatus: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2229 < LEI>
A; Cross-references: EMBL:U42834; NID:g1125756; PID:g1125759; PIDN:AAA83584.1; CESP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted to the EMBL Data Library, April 1997
A; Reference number: 219664
A; Accession: T23053
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2014 <WIZ>A; Cross-references: EMBL: 293779; PIDN:CAB07849.1; GSPDB:GN00028; CESP:T25C12.3
                                                                                                                                                                                                                                                                                                                                                                                                           A; Introns: 60/3; 98/1; 305/3; 326/1; 383/1; 407/1; 471/1; 510/2; 550/3; 598/3;
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hypothetical protein F28B4.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T16199
R;Leimbach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1601 RTFEKYNYTTIDALITDLTAQSTAISTDGACSMPYLGVLAHLLEHDNVISIPNSBIFLVT 1660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypochetical protein T25C12.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T21560; T23053; T25270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1551 TLLFVVETTRQNSDTVNQLIANLKNIVTSA-----TNFA--PFWFSYFGLVTFDTTG 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----TADPVVFQRELRQLYVQGGDCPEMSVGAIKAAVE----VANPGSFIYVFS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 DARAKDYHKKNELLQLLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEE---IASTSSGQVFQL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           199 DKQQVSEVL-KWVESAIQASKVHLLS----ADHE-EEGEHTWRIPFDPSLKEVTISLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    39 TLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Post Local Similarity 20.1%; Pred. No. 1.1;
Matches 52; Conservative 48; Mismatches 119; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: 219441
A; Accession: T21560
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-2014 (AILL)
A; Cross - references: EMBL: 278543; PIDN: CAB01757.1; GS
A; Experimental source: clone F29G6
B; White, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Experimental source: clone H06K08
R:Kershaw, J.
submitted to the EMBL Data Library, November 1995
A:Reference number: 220007
A:Accession: T25270
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Harris, B. submitted to the EMBL Data Library, August 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1778 EFGSLSVKDPLGQAHNVAP 1796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         252 PGPEIEVRDPLGMSQGSPP 270
                                                                                                                                                                                                                                                                                                                                                                                    A; Gene: CESP: F28B4.3
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A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
                                                                                                                                                                        T43290

Chantentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Date: 11-Jan-3200; T0593; T24734
R;Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-A;Reference number: 222396
A;Accession: T43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
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A;Molecule type: DNA
A;Realdus: 1-5198 (WIL)
A;Coss-locations: EMBL: 47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone F15G9
A;Experimental source: clone F15G9
B;Kershaw, J
Submitted to the EMBL Data Library, December 1994
A;Reference number: 219929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TESTGUES: 1-5198 <A12>
Cross references: EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
Experimental source: clone T09B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67 AQREKLIYNYIMVPFHDPYLGEIINTTDSTYFMRQLSKVYVHGGGDCPEKTLTGILKALQ 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 VANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIAS 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 190 TSSGQVFQLDKQQVSEVLKWVESAIQASKVHLLSADHEEEGEHTWRIPFDPSLKEVTISL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.8%; Score 628.5; DB 2;
48.6%; Pred. No. 5.7e-45;
tive 51; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Status: preliminary; translated from GB/EMBL/DDBJ Molecule type: mRNA Residues: 1-5198 <VOG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: BBL:AF074901; PIDN:AAC26792.1 R; Sulston, J. submitted to the EMBL Data Library, December 1994 A; Reference number: 219355 A; A; Reference number: 219355 A; Steussion: T20933 A; Status: preliminary.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SG-----PGPEIEVRDPLG 263
                                               247 SGDKDDSDNLDIVLRDPEG 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 48.6%
Matches 126; Conservative
                SG-----PGPEIEVRDPLG
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T16199
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C; Species: Halobacterium sp. NRC-1
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001
C; Date: 02-Feb-2001
R; NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; La
F; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.,
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A; Atthers: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T
A; Reference number: A84160; MUID: 20504483
                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-1363 <STO>
A; Cross-references: GB:AE004437; NID:g10581390; PIDN:AAG20135.1; GSPDB:GN00138
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein ZK1193.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Coetc.1999 #sequence_revision 15-oct-1999 #text_change 15-oct-1999
C;Accession: T27707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93 TLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFI---YVFSDARAKDYH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AASMAITADATTDTPPLVVVTPSTRTVNQSTDALDVAYRYN-----QPVSGGSAD 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            348 VSMTLAAANGTENATFDISDSPLVANATQRLTLDLAENAPLADGVYTLSVTVDDGSGSPV 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150 KKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLKW 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 ATYTVVAAAVTSDEP----TKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein Vng1953c [imported] - Halobacterium sp. NRC-1
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Best Local Similarity 22.3%; Pred. No. 0.31;
Matches 53; Conservative 49; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riceisel, C. submitted to the EMBL Data Library, November 1995 submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid ZK1193. A; Reference number: Z20409 A; Accession: T27707 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 22/3; 132/1; 182/3; 308/1; 358/3; 403/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7.5%; Score 105.5; D
22.2%; Pred. No. 1.3;
Live 33; Mismatches
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Best Local Similarity 22.2%
Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             A, Accession: C84346
A, Status: preliminary
A, Molecule type: DNA
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                                                                                                            hypothetical
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C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C;Accession: 150726
R;Zhou, M.; Ma, Z.; Sly, W.S.
R;Zhou, M.; Matl. Acad. Sci. U.S.A. 92, 9762-9766, 1995
A;Title: Cloning and expression of the cDNA of chicken cation-independent mannose-6-phos A;Reference number: 150726; MUID:96003859
A;Accession: 150726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-2470 c2RIO>
A;Cross-references: EMBL:U35037; NID:g1019118; PIDN:AAC59718.1; PID:g1019119
C;Superfamily: mannose 6-phosphate receptor, cation-independent; fibronectin type II rep
F;1882-1921/Domain: fibronectin type II repeat homology <2F1>
                                                                                                                                                            69
                                                                                                                         A; Map position: X
A; Introns: 10/2; 91/3; 136/1; 159/2; 182/3; 203/1; 225/3; 280/1; 422/3; 466/3; 559/3;
3; 1722/1; 1779/3; 1843/3; 1908/2; 1941/2; 2007/2
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                                                                                                                                                                                                                                                                                                                    12;
                           EMBL: 266566; PIDN: CAA91487.1; GSPDB: GN00028; CESP: T25C12.3
                                                                                                                                                                                                                                                                                                                                                                                             1580 ------TDLKTK--HK------SYFSFVCKSDAGDDSQPVFLSFDEQ 1612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 ALVPF----HDPDIGPVTLTA---DPVVFQRELRQLYVQG----GGDCPEMSVGAIKAAV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SR-VIANYALVPFHDPDIGPVTLTA----DPVVFQRELRQLYVQGGGDCPEMSVGAIKAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 VEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E---VANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFV---LTGDCGDR-THPGY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                  26 EPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSR-----VIANY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15 YTVVAAAVTSD--EPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRILERSLSSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              182 LAFEEIASTSSGQVFQLDKQQVSE--VLKWV----ESAIQASKVHLLSADHEEEGEHTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52;
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7.6%; Score 106; DB 2; Length 2470;
Best Local Similarity 23.4%; Pred. No. 2.7;
Matches 43; Conservative 30; Mismatches 59; Indels 5
                                                                                                                                                                                                                                                                Length 2014;
                                                                                                                                                                                                                                                           7.8%; Score 109; DB 2; Length 20
23.0%; Pred. No. 1.1;
tive 47; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 RIPFDPSLKEVTISLSGPGPE-IEVRDPLG 263
                                                   A; Experimental source: clone T25C12
                                                                                                                                                                                                                                                                                                              62; Conservative
                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 62; Conservat
A; Residues: 1-2014 <WI3>
                                                                         C;Genetics:
A;Gene: CESP:T25C12.3
                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1613 TCTS 1616
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10;

Gaps

Length 1363;

DB 2; 91; 85

----YAL-VPFHDPDIGPV

10;

Gaps

36;

Length 476;

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A:Molecule type: DNA
A:Residues: 1-1324 <HOS>
A:Cross-references: EMBL:AF016696; NID:g2738764; PID:g2738765; PIDN:AAC01566.1
A:Note: cps-1
C;Superfamily: Mycobacterium tuberculosis mbtE protein; acetate--CoA ligase homoloc C;Keywords: carrier protein; phosphopantethene; phosphoprotean
E:188 -642/Domain: acetate--CoA ligase homology <ACL>
F:659-727/Domain: acyl carrier protein homology <ACC>
F:659-727/Domain: acyl carrier protein (Ser) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    367 TGGRIEIVENTLAVADRTGGEPSLL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 29.20
Lac 42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:U40420; NID:g1065513; PID:g1065514; PIDN:AAA81430.1; CESP:F40FC;Genetics:
A;Gene: CESP:F40F4.6
A;Introns: 57/3; 95/1; 302/3; 323/1; 380/1; 404/1; 468/1; 507/2; 547/3; 595/3; 1532/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F40F4.6 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 20-Sep_1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peride synthetase - Streptomyces fradiae (fragment)
C;Species: Streptomyces fradiae
C;Species: Streptomyces fradiae
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 01-Dec-2000
C;Accession: T14070
R;Hosted, T.J.; Baltz, R.H.
submitted to the EMBL Data Library, July 1997
A;Reference number: 217868
A;Reference number: 217868
A;Accession: T14070
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1717 TDPANIVNLENFYLPTLYGASVLQDPTGITNYTCS-----DGSLPWFVPVDINTTFIYVT 1771
                                              ::||| ::|| |: || |:: : |: |: |: |: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
                                                                                                                                                                                                 1548 SLLMVVETTRQNSDTVNQLIANLKNIVSAVTNNMPLWFTNFGLVTF---DTTGRTFEKFD 1604
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                                                                                                                                               PDIGPVTLTADPVVFQRELRQLYV-QGGGDCPEMSVGAIKAAVEVA----NPGSFIYVFS 141
                                                                                                                                                                                                                                                                                                      DARAK-DYHKKNELLQLLQLKQSQVVFVLT----GDCG-DRTHPGYLAFEEIASTSSGQV 195
                                                                                                                                                                                                                                                                                                                                                                    191 DGTANDDFTTAGFLMEQIVNTRAQILFMITESASGSCNVDVSTNIFESLRSLSQLSRGLL 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDKQQVSEVLKWVESAIQASKV------HLLSADHEEEGEHTWRIPFDPSLKEVTIS 248
           ----RSLSSRSRVIANYALVPFHD 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 FQLDKQQVSEVLKWVESAIQASKVHLLSADHEEEGEHTWRIPF--DPSLKEVTISLSG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 TLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 --TADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVE----VANPGSFIYVFSDARAKDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 HKKNELLQLLQLKQSQVVFVL--TGDCG------DRTHPGYLAFEEIASTSSGQVFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 2214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Pred. No. 2.8;
46; Mismatches 120; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cipencies Canonhabditis elegans Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #texx Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #texx Cibate: 20-Sep-1999 #sequence_revision 20-Sep-1999 #texx B.Wilson, R.Wilson, R.Wilson, R.Wilson, R.Wilson, R. submitted to the EMBL Data Library, November 1995 A:Description: The sequence of C. elegans cosmid F40F4. A:Recession: T16305 A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.5%; Score 105; 19.4%; Pred. No. 2.
ATLAFVFDVTGSMWDDLMQVIDGASRILE----
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Residues: 1-2214 <WIL>
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Matches 51; Conserv
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   38
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A;Note: T17J13.110
C;Superfamily: multidata resistance protein; AfP-binding cassette homology
F;421-615/Domain: AfP-binding cassette homology AABCl>
F;1066-1261/Domain: ATP-binding cassette homology AABC2>
                                                                                                                                   11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------DIGPVTLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVEVAN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            222 VGATLPRERAARILRETAPVCLLTDPDAEAARTRRT-APTGDDRDENAPGGVE---RVVL 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 PGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIASTSS 192
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                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  58 IDG------HDP 87
                                                                                                                                                                                                                              10 LLLATYTVVAAAVTSDEPTKTLSPAT------GDATLAFVFDVTGSMWDDLMQV 57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     278 TGALLAAFDPAPPTDAERAGPLL--------PGHLAYLLHTSGSS
                                                                                                                  97;
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                      Length 1324;
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A;Cross-references: EMBL:AL138651
C;Sxperimental source: cultivar Columbia; BAC clone T17J13
C;Genetics:
7.2%; Score 101.5; DB 2;
20.6%; Pred. No. 2.7;
Live 38; Mismatches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50;
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29.2%; Pred. No. 7.1;
ive 15; Mismatches
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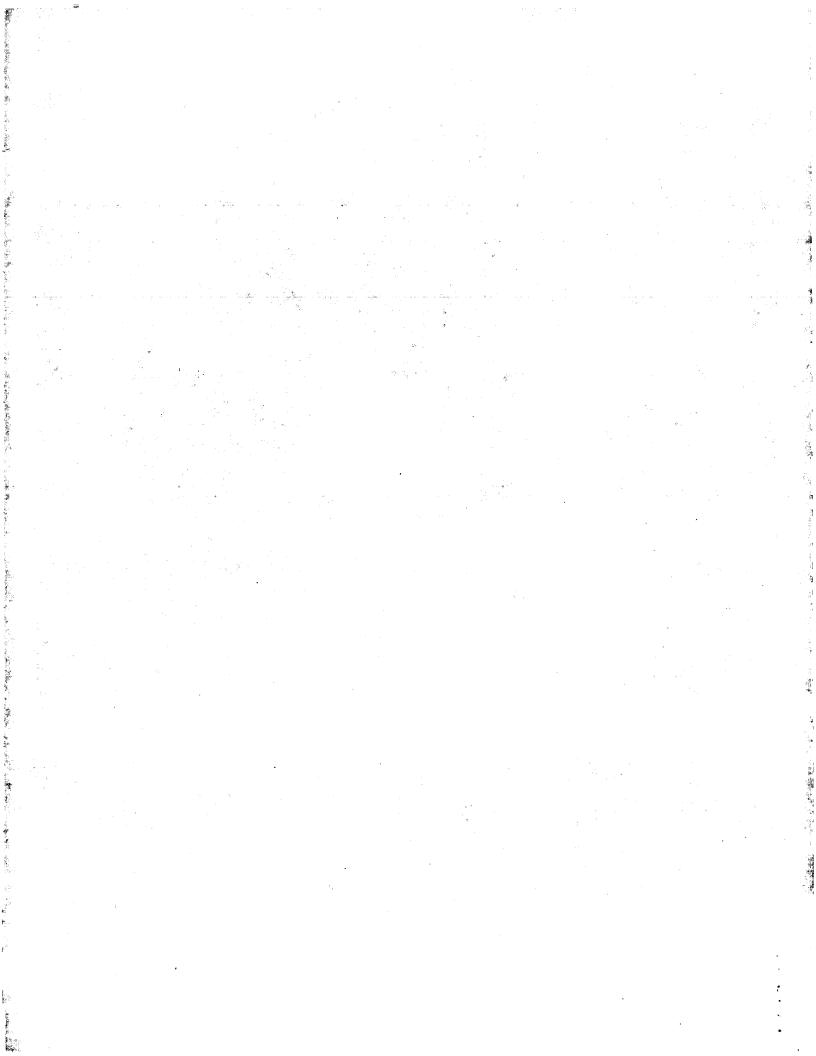
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receptor-like histidine kinase - Rhodococcus erythropolis plasmid pTA421
C; Species: Rhodococcus erythropolis
C; Species: Rhodococcus erythropolis
C; Date: 02-Sep-2000
C; Accession: T30898
C; Accession: T30898
C; Date: 02-Sep-2000
C; Accession: T30898
C; Date: 02-Sep-2000
C; Accession: T30898
C; Access
                                                                                                                                                                                                                                                                                                                                       52 DDIMQVIDGASRILERS-----LSSRSRVIANYALVPFHDPDIGPV-TLTADPVVFQR- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----ELRQLYVQGG-GDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNEL 154
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                                                                                                                                                                        :| :| | | | | | | | | | :| :| | : | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                   DDLMQVIDGASRILERS-----LSSRSRVIANYALVPFHDPDIGPV-TLTADPVVFQR- 103
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                                  75;
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                                      Indels
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Best Local Similarity 24.4%; Pred. No. 17;
Matches 72; Conservative 37; Mismatches 111;
                                      111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein C44H4.1 - Caenorhabditis elegans
ilarity 24.4%; Pred. No. 17;
Conservative 37; Mismatches
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Best Local Similarity
Matches 72; Conserv
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Gene 151, 257-260, 1994
A;Title: The sequence of a cDNA encoding the major vault protein from Rattus norvegicus.
A;Reference number: 153908; MUID:95129871
A;Accession: 153908
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-895 <RES>
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28655
R;Labbe, D.; Garnon, J.; Lau, P.C.
J. Bacteriol. 179, 2772-2776, 1997
A;Title: Characterization of the genes encoding a receptor-like histidine kinase and A;Reference number: 220497; MUID: 97252512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :Species: Rattus norvegicus (Norway rat)
:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999
:Accession: 153908
                                                                                      111 PG--EVLEKDITPLQVVLPNTALHLKALLDFEDKN-GDKVMAGDEWLFE------- 156
                                           -TADPVVFQRELRQLYVQG-G 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: U09870; NID: 9665922; PIDN: AAC52161.1; PID: 9497940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 RVLFAPVRMVTVPPRHYCIVANPVSRDTQSSVLFDITGQVRLRHA-DQEIRLAQDPFPLY 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGASRILERSLSSRSRVIAN----YALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGG 113
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21.7%; Pred. No. 4.7;
iive 43; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                          1150 GDATETE---IVSAAELSNAHGFI 1170
                                                                                                                                                                                                          114 GDCPEMSVGAIKAAVEVANPGSFI 137
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A; Residues: 1-1576 <LAB>
A; Cross-references: EMB::U85412;
A; Experimental source: strain M5
C; Genetics:
A; Gene: bpdS
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Best Local Similarity 21.78
Matches 65; Conservative
                                           VIANYALVPFHDPDIGPVTL-
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673 PEKIIGNTFTVLQKKPEEFRYSEVPFSKDSVGLLITTHITVKGERGEVFKATSYDNYKKV 732
                                                                                  GGDCPEMSVGAIKAAVEVANPGSFI----YVFSDARAKDYHKKNELLQLLQLK----Q 162
                                                                                                                           163 SQVVFVLTGDCGDRTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLKWVESALQASKVHLL 222
                                                                                                                                                                                                                                                                   789 GTLITEIKDIEGDDHGPGNYTY-----ATDKVF------VEHHLDLLKVRLL 829
                                                                                                                                                                                                                                                                                                                                   SADH------SEEGEHTWRIPFDPSLKEVTISL------SGPGPEIEVR 259
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C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Species: Pyrococcus abyssi
C;Accession: A7507
R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Reference number: A75001
A;Reference number: A75001
A;Scatus: preliminary
A;Status: preliminary
A;Status: preliminary
A;Status: C;Axw>
A;Residues: 1-1362 cKAW>
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                                                                                                              Species: Caenorhabditis elegans
:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
.Accession: T19941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLTISNTPIEKVLVFNHDKISYLLFEQMPCYAFQGFQIKKLFLRNNGLRSFH-----PNT 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 LTADPVVFORELROLYVGGG--GDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKK 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 FTGN---LENSLEELEIRGNYIDGIPQSGVSILKQLKILSLPDNLIEYVQDNAFLSYHSR 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152 NELLQLLQLKQSQVVFVLTGDCGDRTHP-GYLAFEEIASTSSGQVFQLDKQQVSEV--- 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 DSLLK-LDLSANNLTAI------HPTGLLGLENLSQLS-----LDKNLLSEIPSQA 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LLATYTVVAAAVTSDEPTKTL-SPATGDATLAFVFDVT---CSMWDDLMQVIDGASRILE 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSLSSRSRV-----IANYALVPFHDPDIGPVT 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
6.6%; Score 93; DB 2; Length 1362;
Best Local Similarity 21.5%; Pred. No. 15;
Matches 65; Conservative 42; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 458;
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OM protein - protein search, using sw model

March 7, 2002, 22:05:27; Search time 26.04 Seconds (without alignments) 387.205 Million cell updates/sec Run on:

US-09-665-728-1 1403 1 WTPRAQLIPILLATYTVVAA.....IEVRDPLGMSQGSPPILLMQD 275

BLOSUM62 Gapop 10.0 , Gapext 0.5 Title: Perfect score: Sequence: Scoring table:

100059 seqs, 36664827 residues Searched: 100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

,	Description				Q9zge6 heliobacill	P26011 mus musculu	Q08189 mus musculu	P38659 rattus norv		Q00248 aspergillus		_	o	_	9 strep	m		-	4	~		_	Q9sjel arabidopsis		_		_	~	7 homo sapi	e	4	7	338 mus m	P09619 homo sapien
SUMMARIES	ID	MVP_RAT	CHLD_SYNP7	PUR4_ARATH	BCHD_HELMO	ITB7_MOUSE	TGL3_MOUSE	PDA4_RAT	STRP_STRSP	PDI_ASPOR	MVP_HUMAN	PGDR_MOUSE	GREA_RHILV	CHLD_TOBAC	STRP_STREQ	PTEN_HUMAN	PTEN_MOUSE	CHLD_PEA	PHS2_DICDI	HMD1_HEVBR	VGLM_BUNYW	SPCB_MOUSE	CHLD_ARATH	AMPH_HUMAN	ATPA_CHLRE	GREA_RHIME	YK58_ARCFU	YAOE_SCHPO	SPCB_HUMAN	ACVS_NOCLA	ATPA_CHLVU	AK_PSEAE	CAD4_MOUSE	PGDR_HUMAN
	DB	1	-	-	Н	7	7	Н	-	~	-	Н	-	-	1	, - 1					-											~	7	П
	Query Match Length	885	677	1387	999	806	693	643	440	515	896	1098	158	758	440	403	403	754	992	575	1433	2128	759	692	202	158	344	1260	2137	3649	206	412	Ч	1106
æ	Query Match		6.7	•	•	•		6.4	•		•				6.3			6.1	6.1	6.1	6.1	9	0.9	0.9	5.9	5.9	5.9	5.9	5.9	5.9	5.8		5.8	5.8
	Score	96	93.5	N	92	91.5	90.5	89.5	88.5	88.5	88		87.5	87	86.5	86	98	85.5	85.5	82	82	84.5	84	83.5	83	82.5	82.5	82.5	82.5	82.5	82	81.5	81.5	81.5
	Result No.		7	m	4	ഹ	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33

Q59007 methanococc	P73077 synechocyst	P09110 homo sapien	058441 pyrococcus	P43503 pseudomonas	P38050 bacillus su	O70309 mus musculu	P48722 mus musculu	P56883 rhizobium m	P55067 rattus norv	005074 haemophilus
YG12_METJA	PARC SYNY3	THIK_HUMAN	SYS_PYRHO	XYLC_PSEPU	PBPF_BACSU	ITB5_MOUSE	OS94_MOUSE	MUTS_RHIME	PGCN_RAT	RFAE_HAEIN
н-		7	7	-	٦	-		Н	Н	Н
411	920	424	455	487	714	798	838	916	1257	476
77 L	0 00	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7	5.7
81	81	80.5	80.5	80.5	80.5	80.5	80.5	80.5	80.5	80

ALIGNMENTS

ALIGNMENTS	RESULT 1 MVP_RAT STANDARD: PRT: 885 AA. TD MVP RAT STANDARD: PRT: 885 AA.	062667; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence u 01-NOV-1997 (Rel. 35, Last annotation MAJOR VAULT PROTEIN (MVP).			norv Gene	INVOIVED IN NUCLEGO-CYTOPLASMIC TRANSPORT. -! SUBUNIT: MAJOR COMPONENT OF THE VAULT, A LARGE RIBONUCLEOPRO PARTICLE. THE VAULT CONTAINS FOUR PROTEINS OF MW 210 KDA, 19 104 KDA AND 54 KDA, RESPECTIVELY, AND A SPECIES OF SMALL RNA CIRCA 140 BASES IN RELATIVE MOMAR RATIOS OF 3:1:55:7:9. -!- SUBCELLULAR LOCATION: CYTOPLASMIC. -!- SIMILARITY: STRONG, TO D.DISCOIDEUM MVPA AND MVPB.	This SWISS-PROT between the Sw the European Bi use by non-pr modified and the entities requir	CRC64;	Query Match 6.8%; Score 96; DB 1; Length 885; Best Local Similarity 21.7%; Pred. No. 2.8; Matches 65; Conservative 43; Mismatches 101; Indels 90; Gaps 16;	QY 4 RAQLLPLLLATYTUVAAAVTSDEPTKTLSPATGDATLAFVEDVTGSMWDDLWQVI 58	QY 59 DGASRILËRSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVPQRELRQLYVQGG 113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6
                                                                                                                                                                                                                                                                                                                                                                                   15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAGNESIUM-CHELATASE SUBUNIT CHLD (MG-PROTOPORPHYRIN IX CHELATASE) (MG-CHELATASE SUBUNIT D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7942.";
(In) Plant Gene Register PGR97-091.
-!- FUNCTION: INVOLVED IN CHLOROPLAST PIGMENT BIOSYNTHESIS; INTRODUCES A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-PROTOROPORPHYRIN IX.
-- PROTOROPORPHYRIN IX.
114 GDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQ---LKQSQVVFV-L 169
                                170 TGDCGDRTHPGYLAFEEIASTSSG----QVFQLDKQQVSEVLKWVESAIQASK--VHLLS 223
                                                                                                                                                                                                            PFHDPDIGPVTL--TADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSF---- 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PFRG-EQAEVLLPPTRSITAARKRLEKMPCGGGLPLAHGLTQAVRVGTNAAQSGDIGQVV 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24 SDEPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGA-SRILERSLSSRSRVIANYALV 82
                                                                                                                   Masuda T., Nakayama M., Ohta H., Takayama K.-I.;
"Cloning and sequencing of a chlD gene encoding a subunit of
magnesium-chelatase from the cyanobacterium Synechococcus sp. PCC
                                                                                                                                                                              224 ADH-----EEEGEHTW-----RIP--FDPSLKEVTISLSGPGPEIEVRDPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- PATHWAY: CHLOROPHYLL BIOSYNTHESIS.
-1- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
-1- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
Bacteria: Cyanobacteria: Chroococcales; Synechococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.7%; Score 93.5; DB 1; Length 677; 4.1%: Pred. No. 3.2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7E2988E096DF5506 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98;
                                                                                                                                                                                                                                                                                                                                              677 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 3.2; 37; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01078; Mg_chelatase; 1.
SMART; SM00327; VWA; 1.
PROSTTE; PS50234; VWRN; 1.
Photosynthesis; Chlorophyll blosynthesis.
DOMAIN 329 383 GLU/PRO.BTCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AB003135; BAA20346.1; -.
InterPro; IPR000523; Mg_chelatse_chII.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 24.18
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          677 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-1140;
                                                                                                                                                                                                                                                                                                                                       CHLD_SYNP7
007345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                          CHLD_SYNP7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
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RY SEQUENCE FROM N.A.

RY THOROLOGIS A. A. ECKET J. R., Palm C.J., Federspiel N.A., Kaul S.,

RY THOROLOGIS A. A. ECKET J. R., Palm C.J., Federspiel N.A., Kaul S.,

RY THOROLOGIS A. A. ECKET J. R., Palm C.J., Fowmen C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowmen C.L., Brooks S.Y.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

ROUND P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fullit C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hulzar L.,

RA Hunter J.L., Jankins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Miltscher J., Miranda M., Niguyen M., Nierman W.C., Osborne B.I.,

RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

R. "Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to licenseéisb-sib.ch).
                                                               IVAITDGRGNIPLARSLGOPMEEGEKPDLKEELLDIAKRIRGLSMOLLVIDT-ERKFVGA 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO TYPE-1 GLUTAMINE
       -----KDYHK---KNELLQLLQLKQSQVVFVLTGDCGDRTHPGY 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATIG74260 OR F1017.7.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Purine blosynthesis; Ligase; ATP-binding; Glutamine amidotransferase;
Chloroplast; Transit peptide.
TRANSIT 1 ? CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last sequence update)
CO-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE PHOSPHORIBOSYLFORWIGLYCINAMIDINE SYNTHASE, CHLOROPLAST
PRECURSOR (EC 6.3.5.3) FGPAM SYNTHASE) (FGAMS) (FORWIGLYCINAMIDE
RIBOTIDE AMIDOTRANSFERASE) (FGARAT) (FORWILGLYCINAMIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLOROPLAST (POTENTIAL).
                                                                                                                                                                         640 GFGKELANAAGGOYYHLPKVSDQAIAAMAQSALRAT 675
                                                                                                                                   LAFEEIASTSSGQVFQLDKQQVSEVLKWVESAIQAS 217
                                                                                                                                                                                                                                                                                                                                                                                   1387 AA.
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AC020579; AAG52403.1; -.
InterPro; IPR000728; AIRS_related.
Pfam; PF00586; AIRS; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMIDOTRANSFERASES.
137 IYVFSDARA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYNTHETASE)
                                                                                                                                                                                                                                                                                                                                                                         PUR4_ARATH
Q9M8D3;
                                                                                                                                                                                                                                                                                                                                            PUR4_ARATH
                                                                   581
                                                                                                                                   182
                                                                                                                                                                                                                                                                                                         RESULT
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us-09-665-728-1.rsp

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                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=99061957; PubMed=8843979;

Xiong J., Inoue K., Bauer C.E.;

"Tracking molecular evolution of photosynthesis by characterization of a major photosynthesis gene cluster from Heliobacillus mobilis.";

Proc. Natl. Acad. Sci. U.S.A. 95:14851-14856(1998).

-! FUNCTION: INVOLVED IN CHLOROPLAST PIGMENT BIOSYNTHESIS; INTRODUCES

A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-
                                                                                                                                                                                                                                                                                                                                                                                                ------AGNKGINLDLASNGISLFETLFSE------ELGLVLEISKTNLDA 1023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1024 VM----EKLRAFDVTAEIIGNVTDSPLIEVKVDGITHLSEKTSFLRDMWEDTSFQLEKL 1078
                                                                                                                                                                                                                                                                                       54 ----IMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLY 109
                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                110 VQGGGDCPEMSVGAIKAAVEVANPGSFIY--VFSDARAKDYHKKNELLQLLQLKQSQVVF 167
                                                                                                                                                                                                                   VVAAAVTSDEPTKTLSP-----53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-NG-2001 (Rel. 40, Last annotation update)
MAGNESIUM-CHELATASE 67 KDA SUBUNIT (MG-PROTOPORPHYRIN IX CHELATASE)
                                                                                                                                                                                                                                                     884 VISAYVTCPDITKTVTPDLKLGGDDGILLHVDLAKGKRRLGGSALAQVFGQIGNDCPDLD
                                                                                                                                                                                                                                                                                                                                                                                                                                    168 VLTGDCGDRTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLK------WVESAIQASKV
                                                                                                                                                                                                                                                                                                               944 DVPYLKNVFDGVQALIAENLVSAG------HDISDGGLVVTALEMAF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROJUKNEVOKHIKIN 1A.
-!- PATHUAY: CHLOROPHYLL BIOSYNTHESIS.
-!- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
-!- SIMILARITY: CONTAINS 1 VWFA DOMAIN.
                                                                                                                                                                                 89;
                  PHOSPHORIBOSYLFORMYLGLYCINAMIDINE
                                                                                                                                           Length 1387;
                                                 ATP (POTENTIAL).
GATASE (BY SIMILARITY).
W; 65E9920DF83F0E95 CRC64;
                                                                                                                                                                               92; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1079 QRLASCVEMEKEGLKFRHEPNWKLSFIPSSTNNNYMSQGMIPKVAV 1124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HLLSA--DHEEEG----EHTWRIPFDPSLKEVTISLSGPGPEIEV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillus/Clostridium group; Heliobacterium group; Heliobacillus.
NCBL_TaxID=28064;
                                                                                                                                             DB 1;
                                                                                                                                                                               52; Mismatches
                                                                                                                                                              Pred. No. 10;
                                                                                                                                           6.6%; Score 92.5; 18.5%; Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF080002; AAC84032.1; -.
InterPro; IPR000523; Mg_chelatse_chII.
InterPro; IPR002035; vWFA.
                                     SYNTHASE
 PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01078; Mg_chelatase; 1.
                                                                                        151778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (MG-CHELATASE SUBUNIT D).
                                                                                                                                                                                 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                    398
1215
1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heliobacillus mobilis.
                                                                                          AA;
                                                                                                                                                                Similarity
                                                    387
1215
1387
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                                                  NP_BIND
ACT_SITE
SEQUENCE
                                                                                                                                             Query Match
                                                                                                                                                                  Local
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 CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                  985
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Sukaryota metazoa, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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P26011; 064656;
01-MAY-1992 (Rel. 22, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INTEGRIN BETA-7 PRECURSOR (INTEGRIN BETA-P); (M290 IEL ANTIGEN).
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MEDLINE=92390425; PubMed=1518854;
Hu M.C.T., Crowe D.T., Weissman I.L., Holzmann B.;
"Cloning and expression of mouse integrin beta p(beta 7): a functional role in Peyer's patch-specific lymphocyte homing.";
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                                                                                                                                                                        36;
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Gurish M.F., Bell A.F., Smith T.J., Ducharme L.A., Wang R.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of the mouse integrin beta 7 subunit.";
J. Biol. Chem. 267:7352-7358(1992).
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Yuan Q., Jiang W.-M., Leung E., Hollander D., Watson J.D.,
Krissansen G.W.;
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                                                                                                                                       DB 1; Length 666;
                                                                                    5CB072BD72072BE5 CRC64;
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18239; pubMed=1710115;
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                                                                                                                                                                        37; Mismatches
            PROSITE: PS50234; VWPA; 1.
Photosynthesis: Chlorophyll biosynthesis.
DOMAIN 475 661 VWFA.
DOMAIN 336 349 POLY-PRO.
                                                                                                                                     6.6%; Score 92; 25.9%; Pred. No.
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J. Immunol. 149:1964-1972(1992).
                                                                                    72578 MW;
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Matches 56; Conservative
SM00327; VWA; 1.
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REMBL; M95632; AAA39323.1; --
REMBL; M95632; AAA39323.1; --
REMBL; S44607; AAB23193.1; --
REMBL; S44607; AAB23193.1; --
REMBL; S63504; AAB23193.1; --
REMBL; S63504; AAB23193.1; --
REMBL; S63504; AAB23196.1; --
REMBL; S63504; AAB23196.1; --
REMBL; S63504; AAB23196.1; --
REMBL; S63504; AAB23196.1; --
REMBL; S46271; A46271
REMBL; S46271; A46271
REMBL; RA4283; AA4283
REMBC; REMO056; EGF-1ike.
RICEPTO; IPRO0369; Integrin_B.
RICEPTO; IPRO0369; PSI
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                            MEDLINE-93305607; Pubmed-8318458;
Leung E., Mead P.E., Yuan Q., Jiang W.M., Watson J.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YISTKAVGSNS-----RMDVTDKYKYPEGSSEERQVHQKALDKLKPNASFGATSSRN 473
                                                                                                    STRAIN-BALB/C; TISSUE-Epidermis; MEDLINE-93286109; PubMed-8099584; Kim I.-G., Gorman J.J., Park S.-C., Chung S.-I., Steinert P.M.; "The deduced sequence of the novel protransglutaminase E (TGase3) of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SVWNFHVWNEGWFVRTDLGPTYNGWQVLDATP-----QERSQGVFQCGPASVNAIKA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                 J. BIOL. Chem. 268:12682-12690(1993).

-!- FUNCTION: CATALYZES THE CROSS-LINKING OF PROTEINS AND THE CONJUGATION OF POLYAMINES TO PROTEINS. IT IS RESPONSIBLE FOR THE LATER STAGES OF CELL ENVELOPE FORMATION IN THE EPIDERMIS AND THE HARR FOLLICLE.

-!- CATALYTIC ACTIVITY: PROTEIN GLUTAMINE + ALKYLAMINE = PROTEIN N(5)-ALKYLGHUTAMINE + NH(3).

-!- COFACTOR: CALCIUM IS REQUIRED FOR TRANSCLUTAMINASE ACTIVITY.

-!- SUBUNIT: THIS ENZYME CONSISTS OF TWO POLYPEPTIDE CHAINS, WHICH SER SYNTHESIZED AS A PRECURSOR FORM OF A SINGLE POLYPEPTIDE.

-!- SIMILARITY: BELONGS TO THE TRANSCLUTAMINASE FAMILY.
                                       Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-DVDRNFDMIFIFAEVNADRITWIYNNRNN----TQKQNSV------DTHSIGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YLAFEEIASTSSGQVFQLDKQQVSEVLKWVESAIQASKVHLLSAD--------HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Indels 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAIN, SECONDAY, TRANSGLUTAMINASES, 1.

Transferase, Acyltransferase, Calcium-binding, Zymogen.

CHAIN 1 470 50 KDA NONCATALYTIC CHAIN.

CHAIN 471 693 27 KDA CATALYTIC CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8B3F0601735D4E84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 90.5; DB
Pred. No. 5.9;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EEGEHTWRIPFDPSL------KEVTISL 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEGEDK ---- EPSISGKFKVTGILAVGKEVSLSL 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GSMWDDLMQVIDGASRILERSLSSRSRVIANY ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:98732; Tgm3.
InterPro; IPR002931; Transglut_core.
InterPro; IPR001102; Transglutmnse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam: PF00927; Transglutamin_C; 1. Pfam: PF00868; Transglutamin_N; 1. Pfam: PF01841; Transglut_core; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29;
                                     Chordata; (Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77324 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; L10385; AAA40421.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00460; TGC;
PROSITE; PS00547; TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    471
273
693 AA;
                                                                                       SEQUENCE FROM N.A
                                                                NCBI_TaxID-10090;
                                                                                                                                                         human and mouse.
           TGM3 OR TGASE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P00488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .
90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PROUGL4; ER_TARGET; 1.
PROSITE; PS00104; ER_TARGET; 1.
PROSITE; PS001094; THIOREDOXIN; 3.
Redox-active center; Isomerase; Endoplasmic reticulum; Repeat; Signal; Glycoprotein; Calcium-binding.
erchar.

20 POTENTIAL.
                                                                                01-FEB-1995 (Rel. 31, Last sequence update)
20-MG-2001 (Rel. 40, Last annoctation update)
PROTEIN DISULFIDE ISOMERASE A4 PRECURSOR (EC 5.3.4.1) (PROTEIN ERP-72)
(ERP72) (CALCIUM-BINDING PROTEIN 2) (CABP2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EUI. J. Biochem. 213:789-795(1993).
-!- CATALYTIC ACTIVITY: REARRANGEMENT OF BOTH INTRACHAIN & INTERCHAIN DISULFIDE BONDS IN PROTEINS TO FORM THE NATIVE STROCTURES.
-!- SUBCELLULAR LOCATION: ENDOPLASMIC RETICULUM LUMEN.
-!- INDUCTION: UPON GLUCOSE STARVATION, AS WELL AS TREATMENT WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---SFIYVFSDARAKDYHKKNEL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15 YTVVAAAVTSDEPTKTLS--PATGDATLAFVFDVTGSMWDDLM---QVIDGASRILERSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      159 VAKVREVS-----QPDWTPPPEVTLTLTKENFDDVVNNADIILVEFYAPWCGHCKKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 SSRSRVIANYALVPFHDPDIGP---VTLTA-----DPVVFQRE--LRQLYVQGGGDCPEM
                                                                                                                                                                                                                         Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
YCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van P.N., Rupp K., Lampen A., Soeling H.-D.; "CaBP2 is a rat homolog of ERp72 with proteindisulfide isomerase activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN DISULFIDE ISOMERASE A4
REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PREVENT SECRETION FROM ER. 85611B66F3A4DE41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- PTM: O-GLYCOSYLATED.
-!- SIMILARITY: CONTAINS 3 THIOREDOXIN DOMAINS.
     643 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.4%; Score 89.5; Di 22.0%; Pred. No. 6.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 SVGAIKAAVEVANPG------
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=WISTAR; TISSUE=Liver;
MEDLINE=93238767; PubMed=8477750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000886; ER_target.
                                                        31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000063; Thiored.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00085; thiored; 3. PRINTS; PR00421; THIOREDOXIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M86870; AAA19217.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72806
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  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         643 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                           [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TUNICAMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEROPS; C17.002;
                                                                                                                                                                                            PDIA4 OR CABP2
                                                        01-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                271 YGIVDYMVEOSGPPSKEILTLKOVO-EFLKDGDDVVILGVFOGVGD----PGYLOYODAAN 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPV------VFQR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 ELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                         Streptococcus sp. (strain 19909).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          155 L-----CGDRTHPGYLAFEEIAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-89160265; PubMed-2922269;
Walter F., Siegel M., Malke H.;
"Nucleotide sequence of the streptokinase gene from a group-G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.3%; Score 88.5; DB 1; Length 440; 25.3%; Pred. No. 4.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREPTOKINASE G.
5521F8825FE1B6EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 VHLLSADHEE-------EGEHTWRIPFDPS-LKEVTI 247
                                                                                                                                                                                                                                     update)
on update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rin; 301/13; 301/13.
Plasminogen activation; Signal; Virulence.
                                                                                                                                                                                                                     01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence up
01-MV-1997 (Rel. 35, Last annotation
STREPTOKINASE G PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           440 S
50199 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X13400; CAA31766.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S02723; S02723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN 27
SEQUENCE 440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=1306;
                                                                                                                                                                                          STRP_STRSP
P10519;
                                                                                              190 T 190
                                                                                                                          327 T 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local
Matches 5
                                                                                                                                                                               STRP_STRSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52
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                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000886; ER_target.
InterPro; IPR000885; Thiored.
InterPro; IPR00085; Thiored.
Pfam; PF00085; thiored.
PROSTIE; PS00194; ER_TARGET; 1.
PROSTIE; PS00194; THIOREDOXIN, 2.
Redox active center; Isomerase; Endoplasmic reticulum; Repeat; Signal.
SIGNAL
                                                                                                                                                                                                          REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
PREVENT SCRETION ER (POTENTIAL).
ALISBA38E20E37EAC CRC64;
                                                                                                                          Eukaryota, Fungi, Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae, mitosporic Trichocomaceae; Aspergillus.
NCBI_TaxID=5062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 LLPLLLATYTVVAAAVTSDEPTKTLSPATGDATLAFVFDVTGSMWDDLM------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 ILSLLGASAVASAADATAEAPSDVVS-LTGDTFETFVKE-----HDLVLAEFFAPWCGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------PDIGPVT-----FORELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 QLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYH---KKNELLQLLQLKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 -----QVIDGASRILERSLS------SRSRVIANY------ALVPFHD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.3%; Score 88.5; DB 1; Length 515;
18.5%; Pred. No. 5.8;
ive 52; Mismatches 109; Indels 117;
                                       01-NOV-1997 (Rel. 35, Created)
1.NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
PROTERN DISULEIDE ISOMERASE PRECURSOR (EC 5.3.4.1) (PDI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN DISULFIDE ISOMERASE
             515 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56458 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; D85900; BAA12913.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63; Conservative
              STANDARD;
                                                                                                              Aspergillus oryzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                515 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-RIB 40;
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M
E
K
             PDI_ASPOR
Q00248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
PDI_ASPOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC, 5% ARE NUCLEUS ASSOCIATED AND LOCALIZE TO THE NUCLEAR PORE COMPLEXES.
TISSUE SPECIFICITY: PRESENT IN MOST NORMAL TISSUES. HIGHER EXPRESSION OBSERVED IN PRITHELIAL CELLS WITH SECRETORY AND EXCRETORY FUNCTIONS, AS WELL AS IN CELLS CHRONICALLY EXPOSED TO EXCRETORY FUNCTIONS, AS WELL AS IN CELLS CHRONICALLY EXPOSED TO XENOMENOTICS, SUCH AS BROWCHIAL CELLS AND CELLS LINING THE INTESTINE. OVEREXPRESSED IN MANY MULTIDRUG-RESISTANT CANCER CELLS. SIMILARITY: STRONG, TO D. DISCOIDEUM WYDA AND MYPB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAT. Med. 1:578-582(1995).

-!- MUCTION: UNKNOWN, THOUGH MYP IS REQUIRED FOR NORMAL VAULT STRUCTURES THAT MAY BE STRUCTURE. VAULTS ARE MULTI-SUBUNIT STRUCTURES THAT MAY BE INVOLVED IN NUCLEO-CYTOPLASMIC TRANSPORT.

-!- SUBUNIT: MAJOR COMPONENT OF THE VAULT, A LARGE RIBONUCLEOPROTEIN PARTICLE. THE VAULT CONTAINS FOUR PROTEINS OF WA 210 KDA, 192 KDA, 104 KDA AND 54 KDA, RESPECTIYELY, AND A SPECIES OF SMALL RNA OF CIRCA 140 BASES IN RELATIVE MOLAR RATIOS OF 3:1:55:7:9 (BY
                            50 --MWDDLMQVIDGASRILERSLSSRSRVIAN----YALVPFHDPDIGPVTLTADPVVFQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42 RVLFAPMRMVTVPPRHYCTVA------NPVSRDAQGLVLFDVTGQVRLRHADLE 89
164 QVVFVLTGDCGDRTHPGYLAFEEIASTSSGQVF---QLDKQQVSEVLKWVESAIQASKVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drug resistance-related protein LRP is the human major vault
                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90; Indels 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 RAQLLPLLLAT ----YTVVAAAVTSDEPTKTLSPATGDATLAFVFDVTGS -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [1]
SEQUENCE FROM N.A.
MEDLINE=96071506; PubMed=7585126;
Scheffer G.L., Wijngaard P.L.J., Flens M.J., Izquierdo M.A.,
Slovak M.L., Pinedo H.M., Meijer C.J.L.M., Clevers H.C.,
                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
1-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%; Score 88; DB 1; Lenyth 896;
21.0%; Pred. No. 14;
Ive 43; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4BADFAEA7C80B7D0 CRC64;
                                                                                   221 LLSADHEEEGEHTWRIPFDPSLKEVTISLSGPGPEIEVRDP 261
                                                                                                                           287 IVTIDAKLYGAHAGNLNLDPS------KFPAFAIQDP 317
                                                                                                                                                                                                                                  896 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        896 AA; 99797 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X79882; CAA56256.1; -. MIM; 605088; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR002499; Vault.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65; Conservative
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Ribonucleoprotein.
SEQUENCE 896 AA; 99797
                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scheper R.J.
                                                                                                                                                                                                                                  MVP_HUMAN
Q14764;
                                                                                                                                                                                                                                                                                                                                                             MVP OR LRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein.
                                                                                                                                                                                        RESULT 10
MVP_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
-!- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
PROTEIN KINASES.
90 IRLAQDPFPLYPG--EVLEKDITPLQVVLPNTALHLKALLDFEDKD-GDKVVAGDEWLFE 146
                                                                                                                                                                           168 IRQNQALRLRARKECWDRDGKERVTGEEWLVTTVGAYLPAVFE-----EVLDLVDAVI 220
                                                                                                                                                                                                                     215 QASK--VHLLSADH------EEEGEHTWRIPFD------PSLKE-----VTISLSGPG 253
                                                                                                                                                                                                                                                        221 LTEKTALHLRARRNFRDFRGVSRRTGEE-WLVTVQDTEAHVPDVHEEVLGVVPITTLGPH 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
20-AUG-2001 (Rel. 40, Last anotation update)
BETA PLAPELET-DERIVED GROWIH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112)
                                                                                               ------GPGTYI-----PRKEVEVVEIIQATI 167
                                                                                                                                      LKQSQVVFV-LTGDCGDRTHPGYLAFEE1ASTSSG----QVFQLDKQQVSEVLKWVESAI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: THIS RECEPTOR BINDS PLATELET-DERIVED GROWTH FACTOR AND HAS A TYROSINE-PROTEIN KINASE ACTIVITY. THIS RECEPTOR BINDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yarden Y., Escobedo J.A., Kuang W.-J., Yang-Feng T.L., Daniel T.O., Tremble P.M., Chen E.Y., Ando M.E., Harkins R.N., Francke U., Fried V.A., Ullrich A., Williams L.T.; "Structure of the receptor for platelet-derived growth factor helps define a family of closely related growth factor receptors."; Nature 323:226-232(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - SUBUNIT: DIMER OF EITHER ALPHA-ALPHA, BETA-BETA OR ALPHA-BETA
                                                            RELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFICALLY TO PDGF-B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1098 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGD; MGI:97531; Pdgfrb.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR00359; Ig_C2.
InterPro; IPR003500; Ig_like.
InterPro; IPR001824; Rcptor_tyr_kin_III.
InterPro; IPR001825; Tyr_kin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Fibroblast;
MEDLINE=87014762; PubMed=3020426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X04367; CAA27882.1; -. PIR; A25742; PFMSRB.
                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                 254 PEIEVRDPLG 263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAVTSDEPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSRVIANY 79
Pfam; PF00047; ig; 4.

SMART; SM0408; 1622; 1.

SMART; SM00401; 1G22; 1.

SMART; SM00219; TYRK; 1.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_TYR; 1.

PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.

TYFOSING-PROTEIN_KINASE_DOM; 1.

TYFOSING-PROTEIN KINASE_DOM; 1.

TYFOSING-PROTEIN KINASE_DOM; 1.

TYROSING-PROTEIN KINASE_DOM; 1.

TYROSING-PROTEIN KINASE_DOM; 1.

TYROSING-PROTEIN KINASE_DOM; 1.

TYROSING-PROTEIN KINASE_DOM; 1.

TYPOSING-PROTEIN KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 VVFVLTGDCGD---RTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLKWVESAIQASKVHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               837 KLVKICDFGLARDIMRDSNYISKGSTYLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         110 VQGGGDCPEMSV----GAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              997 TLGGTPYPELPMNDQFYNAIKRGYRMAQPA--------HASDEIYEIMQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----KCWEEKFETRPPFSQLVLLLERLLGEGYKKKYQQVD-----EEFLRSDHPAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    222 LSADHEEEGEHTWRIPFD-----PSLKEVTISLSGPGPEIEVRDPLGMSQGSPPL
                                                                                                                                                                                 BETA PLATELET-DERIVED GROWTH FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL). (POTENTIAL). (POTENTIAL).
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(POTENTIAL).
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(POTENTIAL).
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18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8D391CAFAC3FC31D CRC64;
                                                                                                                                                                                                                                 CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
PROTEIN KINASE.
ATP (BY SIMILARITY).
                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL)
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18.7%; Pred. No.
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1098
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MOD_RES
CARBOHYD
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BINDING
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Matches
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RESULT 12 GREA_RHILV

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                              "Cloning and overexpression of glycosyltransferases that generate the "Cloning and overexpression of glycosyltransferases that generate the lipopolysaccharide core of Rhizobium leguminosarum.";

J. Biol. Chem. 273:26440(1998).

- I- FUNCTION: NECESSARY FOR EFFICIENT RNA POLYMERASE TRANSCRIPTION ELONGATION PAST TEMPLATE-ENCODED ARRESTING SITES. THE ARRESTING SITES IN DAN HAVE THE PROPERTY OF TRAAPING A CERTAIN FRACTION OF ELONGATION RNA POLYMERASES THAT PASS THROUGH, RESULTING IN LOCKED TERNARY COMPLEXES. CLEAVAGE OF THE NASCENT TRANSCRIP BY CLEAVAGE FACTORS SUCH AS GREA OR GREB ALLOWS THE RESUMPTION OF ELONGATION FROM THE NEW 3'TERMINUS, GREA RELEASES SEQUENCES OF 2 TO 3 NUCLEOTIDES (BY SIMILARITY).
                                                                                                                                                                                                                                                                                           Kadrmas J.L., Allaway D., Studholme R.E., Sullivan J.T., Ronson C.W., Poole P.S., Raetz C.R.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 PGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIASTSS 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 GRISELEDLTARAEVIDLTKMSGDKIKFGAKVKLIDEDTEE--EKTYQIVGDQEADVKAG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9 PGGFVKLQEELRWRQQEERPRIIEAIAEARAH-----GDLSENAE--YHAAKEAQSHNE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         193 GQVFQLD----KQQVSEVLKWVESAIQ-ASKVHLLSADHEEEGEHTWRIPFD--PSLKEV
                                                    30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR
                                                                                                                                              Rhizobium leguminosarum (biovar viclae).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription regulation; DNA-binding; Coiled coil. SEQUENCE 158 AA; 17444 MW; FACA215D8CAF1605 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1;
158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 87.5; DI
Pred. No. 1.4;
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(Rel. 37, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-98434549; PubMed-9756877;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01272; GreA_GreB; 1.
ProDom; PD004918; GreA_GreB; 1.
PROSTITE; PS00829; GREAB_1; 1.
PROSTITE; PS00830; GREAB_2; 1.
                               (Rel. 39, Created)
(Rel. 39, Last sequ
(Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF050103; AAC05214.1; -. HSSP; P21346; 1GRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001437; GreA_GreB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 24.33
Matches 36; Conservative
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                     NCBI_TaxID=387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLD_TOBAC
024133;
15-DEC-1998
15-DEC-1998
                                   30-MAY-2000
GREA_RHILV
                                                                                                             GREA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLD_TOBAC
ID CHLD_T
AC 024133
DT 15-DEC
DT 15-DEC
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g
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us-09-665-728-1.rsp

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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
     STREO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
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                                           a
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                                                                                                                                                                                                                                                            BIOSYNTHESIS; INTRODUCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :| | :: | | : | | : | | :: | | :: | | :: | 542 TDMRAKRAG-ALVIEVVDASGSMALNRWQNAKGAALKLLAESYTSRDQV----CII 596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83 PFHDPDIGPVTLTADPVV--FQRELRQLYVQGGGDCPEMSVGAIKAAVEVANPGS----F 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   597 PFRG-DAAEVLLPPSRSISMARNRLERLPCGGGSPLAHGLTTAVRVGMNAEKSGDVGRIM 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 IVAITDGRANISLKRSTDPEAEASDAPRPSSQELKDEILEVAGKIYKTGMSLLVIDTENK 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---KDYHKKNELLQL------LQLKQSQVV 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-98079235; PubMed-9418040;
Papenbrock J., Gradefe S., Kruse E., Haenel F., Grimm B.;
Mg-chelatase of tobacco: identification of a Chl D cDNA sequence encoding a third subunit, analysis of the interaction of the three subunits with the yeast two-hybrid system, and reconstitution of the enzyme activity by co-expression of recombinant CHL D, CHL H and CHL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDEPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGAS-RILERSLSSRSRVIANYALV 82
                                                     Nicotiana tabacum (Common tobacco), usukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
20-AUG-2001 (Rel. 40, Last annotation update)
MAGNESIUM-CHELATASE SUBUNIT CHLD PRECURSOR (MG-PROTOPORPHYRIN IX
CHELATASE) (MG-CHELATASE SUBUNIT D).
                                                                                                                                                                                                                                                                                                  -i- PATHWAY: CHLOROPHYLL BIOSYNTHESIS.
-i- SUBCELLULAR LOCATION: CHLOROPLAST STROMA.
-i- SIMILARITY: BELONGS TO THE MG-CHELATASE SUBUNITS D/I FAMILY.
-i- SIMILARITY: CONTAINS 1 WWFA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAGNESIUM-CHELATASE SUBUNIT CHLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                167 FVLTGDCGDRTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLKWVESAIQASK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716 FVSTGFA------KEIARVAQGKYYXLPNASDAVISAATKDALSALK 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 758;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93; Indels
                                                                                                                                                                                                                                                            -!- FUNCTION: INVOLVED IN CHLOROPLAST PIGMENT BIOSYNTHE
A MAGNESIUM ION INTO PROTOPORPHYRIN IX TO YIELD MG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ED531E85D5FAFEF8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              biosynthesis; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 87; DB 21.6%; Pred. No. 13; tive 35; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLU/PRO-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000523; Mg_chelatse_chII.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01078; Mg_chelatase; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          434 PC
83012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Photosynthesis; Chlorophyll
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Y10022; CAA71128.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VWFA; 1
                                                                                                                                                                                                                                             Plant J. 12:981-990(1997)
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                                                                                                                                                                                                                                                                                         PROTOROPORPHYRIN IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        427
758 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fransit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            137 IYVFSDARA-
                                                                                                           NCBI_TaxID=4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochemistry 21:6620-6625(1982).

-!- FUNCTION: THIS PROTEIN IS NOT A PROTEASE, BUT IT ACTIVATES PLASMINGERS BY COMPLEXING WITH IT. AS POTENTIAL VIRULENCE FACTOR, IT IS THOUGHT TO PREVENT THE FORMATION OF EFFECTIVE FIBRIN BARRIERS AROUND THE SITE OF INFECTION, THEREBY CONTRIBUTING TO THE INVASIVENESS OF THE CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 DDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPV------VFQR 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDYFEVIDFAS---DATITDRN-----GKVYFADKD-GSVTLPTQPVQEFLLSGHVRVR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     220 ITSQELLAQAQSILNKNHPGYTIYERDSSIVTHDNDIFRTILPMDQEFTYRVKNREQAYR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 ELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQ- 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --SQVVFVLTGDCGDRTHPGYLAFEEIAS--TSSGQVFQLDKQQVSEVLKWVESAIQASK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-83127125; PubMed-6760891;
Jackson K.W., Tang J.;
"Complete amino acid sequence of streptokinase and its homology with
                                                                                                                                                                                                                        Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                            Malke H., Roe B., Ferretti J.J.;
Nuclectide sequence of the streptokinase gene from Streptococcus
equisimilis H46A.";
Gene 34:357-362(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 PYKEKPIQNQA-----KSVDVEYTVQFTPLNPDDDFRPGLKDTKLLKTLAIGDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EKY -> LEYK (IN REF. 2).
N -> D (IN REF. 2).
8FC1F22648ACC77A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219 VHLLSADHEE------EGEHTWRIPFDPS-LKEVTI 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87;
                                                                             01-APR-1988 (Rel. 07, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
STREPTOKINASE C PRECURSOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ပ
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440 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2%; Score 86.5; D
24.9%; Pred. No. 6.9;
ive 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREPTOKINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A00967; BZSO.
PIR; A22801; A22801.
Plasminogen activation; Signal; Virulence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L -> D.
D -> L.
PRT;
                                                                                                                                                                                                                                                                                                                                                                      STRAIN=H46A;
MEDLINE=85232082; PubMed=2989113;
                                                        (Rel. 01, Created)
(Rel. 07, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50140 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; K02986; AAA26974.1; -. EMBL; X72832; CAA51351.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 6.2°
Best Local Similarity, 24.9°
Matches 56; Conservative
                                                                                                                                                                                                   Streptococcus equisimilis
  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     298
438
440 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
SEQUENCE OF 27-440.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=119602;
                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                     21-JUL-1986
STRP_STREQ
P00779;
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000633; 002679; 01.007.00.00633; 002679; 01.007-1997 (Rel. 35, Created) 01.007-1997 (Rel. 35, Last sequence update) 01.007-1997 (Rel. 35, Last sequence update) 01.007-1997 (Rel. 35, Last sequence update) PROTEIN-TYROSINE PHOSPHATASE PTEN (EC 3.1.3.48) (MUTATED IN MULTIPLE ADVANCED CANCERS 1). PREPI. (Released (Human), and Canis familiaris (Dog). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Li J., Yen C., Liaw D., Podsypanina K., Bose S., Wang S.I., Puc J., Milaresis C., Rodgers L., McCombie R., Bigner S.H., Giovanella B.C., Ittmann M., Tycko B., Hibshoosh H., Wigler M.H., Parsons R.; "PTEN, a putative protein tyrosine phosphatase gene mutated in human brain, breast, and prostate cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98007985; PubMed-9345101;
MEDLINE-98007985; PubMed-9345101;
Tsou H.C., Teng D.H.-F., Ping X.L., Brancolini V., Davis T., Hu R.,
Xie X.X., Gruener A.C., Schrager C.A., Christiano A.M., Eng C.,
Steck P., Ott J., Tavtijan S.V., Peacocke M.;
"The role of MMAC1 mutations in early-onset breast cancer: causative
in association with Cowden syndrome and excluded in BRCA1-negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "TEP1, encoded by a candidate tumor suppressor locus, is a novel protein tyrosine phosphatase regulated by transforming growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHARCTERIZATION.

MEDLINE-97404346; PubMed-9256433;

MyGIS M.P., Stolarov J.P., Eng C., Li J., Wang S.I., Wigler M.H.,

Parsons R., Tonks N.K.;

"P-TEN, the tumor suppressor from human chromosome 10q23, is a dual-
specificity phosphatase.";

Proc. Natl. Acad. Sci. U.S.A. 94:9052-9057(1997).
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Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
280 INKKSGLNEEINNTDLISEKYYVLKKGEKPYD-PFDRSHLKLFTI 323
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                                                                                                                     PRT;
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MEDLINE=97228181; PubMed=9072974;
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MEDLINE-97330649; PubMed-9187108;
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MEDLINE-98153621; PubMed-9399897;
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                                                                                                                 STANDARD;
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                                                                           RESULT
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'Germline mutations in PTEN are present in Bannayan-Zonana syndrome.";
Lynch E.D., Ostermeyer E.A., Lee M.K., Arena J.F., J1 H., Dann J., Swisshelm K., Suchard D., MacLeod P.M., Kvinnsland S., Gjertsen B.T., Helmdal K., Lubs H., Moeller P., King M.-C.; "Inherited mutations in PTEN that are associated with breast cancer, cowden disease, and juvenile polyposis.";
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Marsh D.J., Dahia P.L.M., Zheng Z., Liaw D., Parsons R., Gorlin R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-9813933; PubMed-9467011;
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and Bannayan-Zonana syndrome, two hamartoma syndromes with germline
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Chi S.-G., Kim H.-J., Park B.-J., Min H.-J., Park J.-H., Kim Y.-W.,
Dong S.-H., Kim B.-H., Lee J.-I., Chang Y.-W., Chang R., Kim W.-K.,
                                                                                                                                                   VARIANTS CD ARG-123 AND ARG-124.
MEDLINE-87402224; PubMed-9259288;
Nelen M.F., van Staveren W.C.G., Peeters E.A.J., Ben Hassel M.,
Gorlin R.J., Hamm H., Lindboe G.F., Fryns J.-P., Sljmons R.H.,
Woods D.G., Mariman E.C.M., Padberg G.W., Kremer H.;
"Germline mutations in the PTEN/MMACI gene in patients with Cowden disease.";
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Novel mutation of the PTEN gene in an Italian Cowden's disease
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Olschwang S., Serova-Sinilnikova O.M., Lenoir G.M., Thomas G.;
"PTEN germ-line mutations in juvenile polyposis coli.";
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Gastroenterology 115:1084-1089(1998).
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MEDLINE-98408002; Pubmed-9735393;
Scala S., Bruní P., Lo Muzio L., M
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PROTEIN TYROSINE + ORTHOPHOSPHATE.

-1- DISEASE: MUTATIONS OF PTEN ARE FOUND IN A LARGE NUMBER OF CANCERS.
-1- DISEASE: DEFECTS IN PTEN ARE FOUND IN A LARGE NUMBER (CS), ALSO
-1- DISEASE: DEFECTS IN PTEN ARE A CAUSE OF COMDEN SYNDROME (CS), ALSO
-1- DISEASE: DEFECTS IN PTEN ARE A CAUSE OF COMDEN SYNDROME OF SIGNAL DOMINNAT CANCER
-1- PREDISPOSITION SYNDROME ASSOCIATED WITH ELEVATED RISK FOR TUMORS
OF THE BREAST, THYROID AND SKIN. THE PREDOMINANT PHENOTYPE FOR CS
-1- SMULTIPLE HAMARTOMA SYNDROME, IN MANY ORGAN SYSTEMS INCLUDING
--- THE BREAST (70% OF CS PATIENTS), THYROID (40°60%), SKIN, CNS
--- (40%), GASTROINTESTINAL TRACT. AFFECTED INDIVIDUALS ARE AT AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marsh D.J., Kum J.B., Lunetta K.L., Bennett M.J., Gorlin R.J.,
Ahmed S.F., Bodurtha J., Crowe C., Curtis M.A., Dasouki M., Dunn T.,
Feit H., Geraghty M.T., Graham J.M. Jr., Hoddson S.V., Hunter A.,
Korf B.R., Manchester D., Miesfeldt S., Murday V.A., Nathanson K.L.,
Parisi M., Pober B., Romano C., Tolmie J.L., Trembath R., Winter R.M.,
"PTEN mutation spectrum and genotype phenotype Correlations in
Bannayan Riley-Ruvalcaba syndrome suggest a single entity with Cowden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INCREASED RISK OF BOTH BREAST AND THYROID CANCERS. TRICHILEMMOMAS (BENIGN TUMORS OF THE HAIR FOLLICLE INFUNDIBULUM), AND
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DISEASE: DEFECTS IN PTEN ARE A CAUSE OF BANNAYAN-ZONANA SYNDROME
(BRS), ALSO KNOWN AS RUVALCABA-RILEY-SMTH OR BANNAYAN-RILEY-
RUVALCABA SYNDROME (BRRS). IN BLS THERE SEEMS NOT TO BE AN
INCREASED RISK OF MALLGUANAY. IT HAS A PARTIAL CLINICAL OVERLAP
WITH CS. BRR IS CHARACTERIZED BY THE CLASSIC TRIAD OF
MACROCEPHALY, LIPOMATOSIS AND PIGMENTED MACULES OF THE GLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANTS B2S ASP-34; HIS-68; TYR-105; VAL-135; ARG-170 AND LEU-246.
MEDLINE-99330553; PubMed-10400993;
                                                           MEDLINE-99115112; PubMed-9915974; MEDLINE-99115112; PubMed-99155114; Matsunaka T., Takada Y., Emi M.; Kurose K., Araki T., Matsunaka T., Takada Y., Emi M.; "Variant manifestation of Cowden disease in Japan: hamartomatous polyposis of the diseastive tract with mutation of the PTEN gene."; Am. J. Hum. Genet. 64:308-310(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peeters E.A.J., Padberg G.W.;
"Novel PPEN mutations in patients with Cowden disease: absence of
clear genotype-phenotype correlations.";
Eur. J. Hum. Genet. 7:267-273(1999).
                                                                                                                                                                                                                                                                                                       "Severe Lhermitte-Duclos disease with unique germline mutation of
                                                                                                                                                                                                                                  MEDLINE-99158469; PubMed=10051160;
Sutphen R., Diamond T.M., Minton S.E., Peacocke M., Tsou H.C.,
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MEDLINE-99250761; PubMed-10234502;
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Genet. 18:12-14(1998)
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                                              VARIANT CD GLN-130.
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Gaps

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283 PEETSEKVENGSLCDGIDSICSIERADNDKEYL------VLTLTKNDLDKANKDKA 333
172 -- DCGDRTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLKWVESAIQASKVHLLSADHEEE 229
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	076518 caenorhabdi	Q9ump9 homo sapien	Q9y334 homo sapien	Q9z1q8 mus musculu	Q9jha8 mus musculu	Q9qxel mus musculu	Q19853 caenorhabdi	Q22774 caenorhabdi	Q90681 gallus gall	Q9hnt5 halobacteri	Q23410 caenorhabdi	Q20219 caenorhabdi	O52048 streptomyce	Q9mlq9 arabidopsis	005201 rhodococcus	069354 rhodococcus	Q93377 caenorhabdi	Q9eqk5 mus musculu	Q9v294 pyrococcus
SOMETHING	ID	076518	Q9UMP9	Q9Y334	092108	Ф9ЛНАВ	Q9QXE1	Q19853	022774	090681	Q9HNT5	023410	Q20219	052048	09M1Q9	005201	069354	093377	Q9EQK5	09V294
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ď	Query Match	44.8	20.1	20.1	20.1	20.1	8.3	7.8	7.8	7.6	7.5	7.5	7.5	7.2	6.9	6.7	6.7	9.9	9.9	9.9
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ALIGNMENTS

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LVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVF 140
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                                                                                                                                                                                                                             Albertella M.R.; Thesis (1997). University of Oxford, Department of Biochemistry, MRC Immunochemistry Unit. EMBL; AJ245418; CAB52192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                   20.1%; Score 282.5; DB 4; Length 29.2%; Pred. No. 1.3e-15; ive 50; Mismatches 93; Indels
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Best Local Similarity 29.2'
Matches 79; Conservative
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Best Local Similarity 29.4.
Best Toy, Conservative
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536 AA;
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SEQUENCE
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PROSITE: PSG010; BPD_TRANSP_INN_MEMBR; UNKNOWN_1.
PROSITE: PSG1186; EGF_2; UNKNOWN_1.
PROSITE: PSG1187; EGF_CA: 2.
Alternative splicing; Calcium-binding; EGF-like domain; Glycoprotein; Repeat; Signal 1 24 POTENTIAL.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Albertella M.R., Campbell R.D.;
Albertella M.R., Campbell R.D.;
Characterisation of the novel gene G7c located in the class III
region of the human Major Histocompatibility Complex.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
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1462 5198 MISSING (IN ISOFORM F15G9.4A)
5198 AA; 570816 MW; DA8511FF2B58B37B CRC64;
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Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
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Last annotation update)
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44.8%; Score 628.5; DB 5;
Best Local Similarity 48.6%; Pred. No. 1.7e-43;
Matches 126; Conservative 51; Mismatches 69;
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InterPro; IPR000515; BPD_transp.
InterPro; IPR000561; EGF-1ike.
InterPro; IPR001881; EGF_Ca.
InterPro; IPR003598; Ig_Ca.
InterPro; IPR003500; Ig_like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR002035; vWFA.
Pfam; PF00047; Ig; 47.
           BPD_transp.
                                                                                                                                                                        SMART; SM00179; EGE_CA; 1.
SMART; SM00001; EGE_IIke; 1.
SMART; SM00408; IGC2; 44.
SMART; SM00410; IG_IIke; 3.
SMART; SM00327; VWA; 1.
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
G7C PROTEIN (FRAGMENT).
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SEQUENCE FROM N.A.
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117

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Gaps

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ь. Г Gaps 25 DEPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSR----VIANYA 80 SEQUENCE FROM N.A. SEQUENCE FROM N.A. Old S., Madan A., Hicks Nowen L., Old S., Madan A., Abbasi N., Shaffer T., Hood L.; Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.; Requence of the human major histocompatibility complex class III Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606; 49; 20.1%; Score 282.5; DB 4; Length 852; 29.2%; Pred. No. 2.5e-15; ive 50; Mismatches 93; Indels 49 (MAR-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF134726; AAD21820.1; -. SEQUENCE 852 AA; 92538 MW; 025430B3F912A941 CRC64; 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)

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Last sequence update)
Last annotation update)

Created)

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Snoek M., Teuscher C., van Vugt H.; "Molecular analysis of the major MHC recombinational hot spot located within the G7c gene of the murine class III region that is involved in
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                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/RIJ, AND BALB/C; TISSUE=BRAIN;
MEDLINE=20260998; PubMed=10803853;
Snock M., Albertella M.R., van Kooij M., Wixon J., van Vugt H.,
de Groot K., Campbell R.D.;
"G7c, a novel gene in the mouse and human major histocompatibility
complex class III region, possibly controlling lung tumor
                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_TaxID=10090;
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Mus musculus (Mouse).
Eukaryota; Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.1%; Score 282.5; DB 11; Length 891; 30.3%; Pred. No. 2.7e-15; ive 45; Mismatches 100; Indels 41;
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Last annotation update)
                                                                                                                                                                                                                                                                STRAIN=C57BL/RIJ, AND BALB/C; TISSUE=BRAIN;
MEDLINE=98211706; PubMed=9551980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 -LKEVTISLSGPGPEIEVRDPLGMSQG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               525 LLWQVTVRMHGDISSFWIKSPAGVSQG 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   susceptibility.";
Immunogenetics 51:383-386(2000).
EmbL; AF134318; AAF69177.1; -.
EMBL; AF134319; AAF61401.1; -.
InterPro; IPR002035; vWFA.
                                                                                                                                                                                                                                                                                                                                                               disease susceptibility.";
J. Immunol. 160:266-272(1998).
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                                         01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
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Matches 81; Conservative
      PRELIMINARY;
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SMART; SM00327; VWA;
SEQUENCE 891 AA; 9
                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                      G7C (G7C PROTEIN)
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                        09ЛНАВ;
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                                                          476 GGEVIFTKDQHIRDVAAIVGESMAA----LVT------LPLDPPVVVPGQPLVF 519
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301 DRDFSRLLDITPASSLSFVLDTTGSMGEI-----NAAKIQARHLVEQRRGSPMEPVHYV 355
                                       LVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVEVANPGSFIYVF 140
                                                                                                                    141 SDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCG---DRTHPGYLA-----FEEIASTS 191
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                                                                                                                                                                                                 192 SGQVFQLDKQQVSEVLKWVESAIQASKVHLLSADHEEEGEHTWRIPFDPS------
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             196 FQLDKQQVSEVLKWVESAIQASKVHLLSADHEEEGEHTWRIPFDPS-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rowen L., Madan A., Qin S., Shaffer T., Ratcliffe A., Abbasi N., Dickhoff R., James R., Loretz C., Lasky S., Hood L.; "Sequence of the mouse major histocompatibility locus class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.1%; Score 282.5; DB 11; Length 873; 30.3%; Pred. No. 2.6e-15; ive 45; Mismatches 100; Indels 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF109905, AAC84152.1; -
InterPro; IPR002035; vWFA.
SMART; SM00327; vWFA. 1.
Hypothetical protein.
SEQUENCE 873 AA; 94894 MW; 5761E3620F8D831C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY.1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHERICAL 94.9 KDA PROFEIN.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                          873 AA
                                                                                                                                                                                                                                                                                                         520 SVDGLLQKITVRIHGDISSFWIKNPAGVSQG 550
                                                                                                                                                                                                                                                                              242 ----LKEVTISLSGPGPEIEVRDPLGMSQG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 -LKEVTISLSGPGPEIEVRDPLGMSQG 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLWQVTVRMHGDISSFWIKSPAGVSQG 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            489 IFTKDQYIQD----VAAIVGESMAGLVT---
                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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Best Local Similarity 30.3%
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
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MEDLINE—90150718; Pubmed—7906388;
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Milson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Monfaeld J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Ratcon M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Carton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
A Gardner A., Green P., Mirsten T., Jaister M., Latrellle P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
A Barsonia J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Ramaldon N., Smith A., Sonnhammer E., Staden R., Watsen A., Waterston R.,
A Hierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
A Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
elegans ".,
                                                                                                                                                                                                                                                                                                                                                                      64 PPPSLLRPPPVLLATVRYLAGEVA------GRGDVSCAEVASFVADRLRAVRLDLS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                   105 -LRQLYVQGGGDCP-------EMSVGAIKAAVEVANPGSFIYVFSDARAK 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         164 SLRRCYARGKGPYPRQAAFQGLFLLYNLGSLEAPAGGSTAALRACPPLQAALAVDAAFRE 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                224 DNHARLFRLIRTLPYLOS------CAVQEHIGYARRKALARLSRALSTPKGQTLPLD 274
                                                                                                                                                                                                                                                                                                                                                                                                           55 MQVID--GASRILERSLSSRSRVIANYALVPFHDPDIGPVTL--TADPVVFQRE----- 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                    Yoshida M., Kuwahara K., Sakaguchi N.;
"Molecular cloning of a novel gene, SHD-1, belonging to cell cyclerelated SAC3 family."
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ131957; CAB65242.1; -.
SEQUENCE 353 AA; 38203 MW; D486B7B301493447 CRC64;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147 DYHKK-NELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIA-----STSSGQVFQLD
                                                                                                                                                                                                                                                                                                                                    3 PRAQLL---PLLLATYTVVAAAVTSDEPTKTLSPATGDATLA----FVFDVTGSMWDDL-
                                                                                                                                                                                                                                                             Length 353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 FIEHFLALDGLQEARDLCQAHGLTLDKDRVVFLRGQYSEEG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update
NCBI GI: 1125759.
                                                                                                                                                                                                                                                         8.3%; Score 116; DB 11;
ilarity 24.9%; Pred. No. 0.089;
Conservative 31; Mismatches 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2229 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 70; Conserv
                                                                  FROM N.A.
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Q19853
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1601 RTFEKYNYTTIDALITDLTAQSTAISTDGACSMPYLGVLAHLLEHDNVISIPNSEIFLVT 1660
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1551 TLLEVVETTRONSDTVNQLIANLKNIVTSA-----TNFA--PFWFSYFGLVTFDTTG 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEE---IASTSSGQVFQL 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----TADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVE----VANPGSFIYVFS 141
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Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: WEAK, TO C.ELEGANS 2K1193.2 AND TO THE C-TERMINAL OF
COLLAGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 TLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DKQQVSEVL-KWVESAIQASKVHLLS----ADHE-EEGEHTWRIPFDPSLKEVTISLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Score 110; DB 5; Length 22; Pred. No. 4.4; 48; Mismatches 119; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   873C82B6A97AEA25 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 221.3 KDA PROTEIN T25C12.3 IN CHROMOSOME X.
                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50041; C_TYPE_LECTIN_2; 1. PROSITE; PS00022; EGF_1; UNKNOWN_6. PROSITE; PS01186; EGF_2; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q22774; 001703; 001984;
01-3An-1999 (TrEMBLrel 05, Created)
01-3Ar-1999 (TrEMBLrel 10, Last seq
01-JUN-2001 (TrEMBLrel 17, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, 266566; CAA91487.1; -.
EMBL, 278543; CAA91487.1; JOINED.
EMBL, 293779; CAA91487.1; JOINED.
EMBL, 293779; CAB07849.1; -.
EMBL, 278543; CAB07849.1; JOINED.
EMBL, 266566; CAB07849.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00022; EGF_1; UNKNOWN, PROSITE; PS01186; EGF_2; 3. PROSITE; PS50234; VWFA; 1. EGF-11ke domain; Glycoprotein, SEQUENCE 2229 AA; 244874 MW;
Submitted (DEC-1995) to the EMBL. U42844, AAA83584.1; - InterPro: IPR000142; C. InterPro: IPR000561; EGF-1ike. InterPro: IPR001304; lectin_c. InterPro: IPR001304; lectin_c. Pfam; PF00008; EGF; 2. Pfam; PF00009; Lectin_c: IPR00059; lectin_c: IPR00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00111; C4; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 3.
SMART; SM00327; VWA; 1.
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Best Local Similarity 20.1%
Matches 52; Conservative
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                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                      80 ALVPF----HDPDIGPVTLTA---DPVVFQRELRQLYVQG----GGDCPEMSVGAIKAAV 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TTEMBLEEL. 01, Created)
01-NOV-1996 (TTEMBLEEL. 01, Last sequence update)
01-UNV-1996 (TTEMBLEEL. 01, Last sequence update)
01-UNN-2001 (TTEMBLEEL. 01, Last sequence update)
CATION-INDEPENDENT MANNOSE-6-PHOSPHATE RECEPTOR.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria, Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                               26 EPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSR-----VIANY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=96003859; PubMed=7568213; Zhou M., Ma Z., Sly W.S.; "Cloning and expression of the cDNA of chicken cation-independent
                                                                                                                                                                                                                                                                                                             129 E---VANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFV---LTGDCGDR-THPGY
                                                                                                                                                                                                                                                                                                                                                   182 LAFEEIASTSSGQVFQLDKQQVSE--VLKWV----ESAIQASKVHLLSADHEEEGEHTW
                                                                                                                                                                                                             44;
                                                                                                                                                                                          Length 2014;
                                                                                                                                                                                        Similarity 23.0%; Score 109; DB 5; Length 20 Similarity 23.0%; Pred. No. 4.6; Conservative 47; Mismatches 117; Indels
                                                                                                                                                  Hypothetical protein.
SEQUENCE 2014 AA: 221261 MW; 65E3BC76440C73BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mannose-6-phosphate receptor...;
Proc. Natl. Acad. Sci. U.S.A. 92:9762-9766(1995).
BMBL; U35037, Ac59718.1;
HSSP; P02751; ZRN2.
InterPro: IPR000479; CIMR_repeat.
InterPro: IPR000562; FN_TYPe_II.
InterPro: IPR000917; Sulfatase.
Pfam; PF000878; CIMR_repeat; 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2470 AA.
                                                                                                                                                                                                                                                                                                                                                                                                   235 RIPFDPSLKEVTISLSGPGPE-IEVRDPLG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00013; FNTYPEII.
ProDom; PD000995; FN_TYPE_II; 1.
                                                                                                                                                                                                             62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                             407
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                                                                                                                                                                                                                                                                                                                                                                                   73 SR-VIANYALVPFHDPDIGPVTLTA----DPVVFQRELRQLYVQGGGDCPEMSVGAIKAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 VEVANPGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEI 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                       15 YTVVAAAVTSD--EPTKTLSPATGDATLAFVFDVTGSMWDDLMQVIDGASRILERSLSSR 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----YAL-VPFHDPDIGPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                       1533 AKSSCANGAAVCITD---GPKTLNAGKLSKTLTYEDQVLKLVYEDGDPCP-----
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                                                                                                                                                               DB 13; Length 2470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteriales; Halobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                    PROSITE; PS00023; FIBRONECTIN_2; UNKNOWN_1.
PROSITE; PS00149; SULFATASE_2; UNKNOWN_1.
SEQUENCE 2470 AA; 275645 WW; DB33824479CDA1A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Complete proteome.
SEQUENCE 1363 AA; 138692 MW; A34770E00AAA5A58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---SRSRVIAN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1363 AA
                                                                                                                                                                                                                30; Mismatches
                                                                                                                                                               7.6%; Score 106; D 23.4%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                               Query Match 7.6%
Best Local Similarity 23.4%
Matches 43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
SMART; SM00059; FN2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Halobacterium.
NCBI_TaxID=64091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1613 TCTS 1616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188 ASTS 191
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MEDLINE-94150718; PubMed-7906398;
MISON R., Alnscough R., Anderson K., Baynes C., Berks M.,
Milson R., Alnscough R., Anderson C., Berks M.,
Acraton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Acardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
A Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Ranaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
And Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Attson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
Matson A., Meinstock L., Wilkinson-Sproat J., Mohldman P.,
150 KKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLKW 209
               PDIGPVTLTADPVVFQRELRQLYV-QGGGDCPEMSVGAIKAAVEVA----NPGSFIYVFS 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 DARAK-DYHKKNELLQLLQLKQSQVVFVLT----GDCG-DRTHPGYLAFEEIASTSSGQV 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | | : : : : | | : | DGTANDDFTTAGFLMEQIVNTRAQILFMITESASGSCNVDVSTNIFESLRSLSQLSRGLL 250
                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQLDKQQVSEVLKWVESAIQASKVHLLSADHEEEGEHTWRIPF--DPSLKEVTISLSG 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38 ATLAFVFDVTGSMWDDLMQVIDGASRILE------RSLSSRSRVIANYALVPFHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49; Mismatches 100; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.;
Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; 441553, AA483292.1, .
InterPro; IPR000561; EGF-11ke.
SWART; SW00181; EGF; 1.
PROSITE: PS00022; EGF-1, UNKNOWN_2.
PROSITE: PS01186; EGF-2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                         01, Last sequence update)
17, Last annotation update)
REGION TO TENASCIN PRECURSORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-11ke domain; Glycoprotein.
SEQUENCE 476 AA; 53310 MW; F39C14163CC074DA CRC64;
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                                                                                                                                                    476 AA.
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                                                                                                                                                                               Created)
                                                                                                                                                    PRT;
                                                     VESAIQASKVHLLSADHEEEG 230
                                                                             502 VREVIDNSNYTVYVTATDERG 522
                                                                                                                                                                            01, 0
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Best Local Similarity 22.33
Matches 53; Conservative
                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                           01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
                                                                                                                                                                                                                 SIMILARITY OVER A SHORT
                                                                                                                                                                                                                                           Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                       NCBI_TaxID=6239;
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                                                                                                                                                                023410;
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SEQUENCE FROM N.A.

MISON R., Alderson K., Baynes C., Berks M.,
Milson R., Alnscough R., Anderson K., Baynes C., Berks M.,
Milson R., Alnscough R., Anderson R.,
Bonfleld J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Carden A., Green P., Hawkins T., Hiller L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightuing J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riffen L., Roopra A., Saunders D., Shownkeen R.,
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Arierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Misson A., Welnstock L., Wilkinson-Sproat J., Wohldman P.,
Elegans.,
Telegans.,
Telegans.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoldea; Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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39 TLAFVFDVTGSMWDDLMQVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTL---- 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston R.; Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 12;
                                                                                                                                                                                                                                   01-NOV-1996 (TrEMBLrel. 01, Last sequen 01-JUN-2001 (TrEMBLrel. 17, Last annota CODED FOR BY C. ELEGANS CDNA YK131E8.3.
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                                                                                                                                                                                                                Created)
                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U40420; AAA81430.1; InterPro; IPR000561; EGF-11ke. InterPro; IPR0001304; Lectin_c. InterPro; IPR002035; vWFA. Pfam; PF00008; EGF; 2. Pfam; PF00059; Lectin_c; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00092; vwa; 1.
SMART; SM00034; CLECT; 1.
SMART; SM00181; EGF; 3.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51; Conservative
                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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005201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
1665 GNYVETMEVLFNTQAHLHYVVSKTANCATFDGVNNVRDMTWLGY------GSSGNILF 1716
                                           1717 TDPANIVNLFNFYLPTLYGASVLQDPTGITNYTCS-----DGSLPWFVPVDINTTFIXVT 1771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----DIGPVTLTADPVVFQRELRQLYVQGGGDCPEMSVGAIKAAVEVAN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |: :: ||: :| |: : | :: | 315 GRPKGVAVEHAQVTALLSWAGTGVGADRLHRTVASTSES------FDVSVFDTLVPLL 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 LLLATYTVVAAAVTSDEPTKTLSPAT------GDATLAFVFDVTGSMWDDLMQV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102 LLERALTAVHSAPATPTAALAATPATARAAPRAAGPGAPATIVDAFEARVRATPEAPAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58 IDG------HDP-----HDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : || || || || 222 VGATLPRERAARILRETAPVCLLTDPDAEAARTRRT-APTGDDRDENAPGGVE---RVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133 PGSFIYVFSDARAKDYHKKNELLQLLQLKQSQVVFVLTGDCGDRTHPGYLAFEEIASTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      278 TGALLAAFDPAPPTDAERAGPLL--------PGHLAYLLHTSGSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193 GQV--FQLDKQQVSEVLKWVESAIQASKVHLLSADHEEEGEHTWRIPFDPSLKEVTISLS
                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomyces.NCBI_TaxID=1906;
              LDKQQVSEVLKWVESALQASKV------HLLSADHEEEGEHTWRIPFDPSLKEVTIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 1324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1324 1324
1324 AA; 140539 MW; 24285EDD3690964F CRC64;
                                                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                Hosted T.J., Baltz R.H.;
Submitted (JUL-1997) to the EMBL/GenBank/DDBJ datab.
BMBL; AF016696; AAC01566.1; --
HSSP; P14687; AAWU.
InterPro: IPR000873; AMP-bind.
InterPro: IPR001880; Phosphopant_attach.
Pfam; PF00550; AMP-binding; 1.
Pfam; PF00550; AMP-binding; 1.
Pfam; PF00550; Pp-binding; 1.
PRINTS; PR00154; AMPHINDING,
PROSITE; PS00755; ACP_DOWAIN; 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38; Mismatches 123;
                                                                                                                                                                   PRT; 1324 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 7.2%; Score 101.5; Best Local Similarity 20.6%; Pred. No. 11; Matches 67; Conservative 38; Mismatches
                                                                                                                                                                                           01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last seque
01-JUN-2001 (TrEMBLrel. 17, Last annot
PEPTIDE SYNTHETASE MODULE (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPGPEIEVRDPLGMSQ---GSPPLL 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            367 TGGRIEIVENTLAVADRTGGEPSLL 391
                                                                                         1772 TSAEFGSLSVKDPLGAAHSATPV 1794
                                                                           249 LSGPGPEIEVRDPLGMSQGSPPL 271
                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                          Streptomyces fradiae.
                                                                                                                                                                                                                                                                                                                           FROM N.A.
                                                                                                                                                                                                                                                                                                                                      STRAIN-A54145;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                   052048
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-----TADPVVFQRELRQLYVQG-G 113
                                                                                                     T1713.110.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Core eudicots; Rosidae;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 SDEPTKTLSPATGDATLAFVF-----DVTGSMWDDLMQVIDGASRI--LERSLSSRSR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (ABC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rhodococcus sp.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
NCBI_TaxID=1831;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 1292;
                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Mewes H.W.,
Lemcke K., Mayer K.F.X., Quetler F., Salanoubat M.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY
TRANSPORTERS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9C95DF3AC84E7432 CRC64;
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01-Jul-1997 (TrEMBLrel. 04, Last sequence update)
01-Jul-2001 (TrEMBLrel. 17, Last annotation update)
RECEPTOR-LIKE HISTIDINE KINASE BPDS.
                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.9%; Score 96.5; DB 10;
29.2%; Pred. No. 27;
tive 15; Mismatches 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL, AL138651; CAB71875.1; -.
InterPro; IPR0013593; AAA.
InterPro; IPR001140; ABC_transporter_tmem.
InterPro; IPR0011640; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR00155; C5_DNA_meth.
Pfam; PF00064; ABC_membrane; 2.
Pfam; PF00005; ABC_tran; 2.
SMART; SM00382; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PSO0211; ABC_TRANSPORTER; 2.
PROSITE; PS00095; C5_WTASE_2; UNKNOWN_1.
ATP-bind; Transport.
SEQUENCE 1292 AA; 139753 MW; 9C95DF3.
        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 GDCPEMSVGAIKAAVEVANPGSFI 137
01-0CT-2000 (TrEMBLrel. 15, 01-0CT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17, P-GLYCOPROTEIN-LIKE PROETIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 VIANYALVPFHDPDIGPVTL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 42; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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15;
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Best Local Similarity 24.4%; Pred. No. 66;
Matches 72; Conservative 37; Mismatches 111; Indels 75; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 DDLMQVIDGASRILERS-----LSSRSRVIANYALVPFHDPDIGPV-TLTADPVVFQR- 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104 -----ELRQLYVQGG-GDCPEMSVGAIKAAVEVANPGSFIYVFSDARAKDYHKKNEL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  247 QTAEEALGELEALMATGGDGTPPKGLLPRSDRAVPAAEPPL------VGRHTEL 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   155 LQLLQLKQSQV----VFVLTGDCGDRTHPGYLAFEEIASTSSGQVFQLDKQQVSEVLKW 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MTPRAQLLPLLLATYTVVAAAVTSDEPTKTL-----SPATGDATLAFVFDVTGS---MW 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          210 VESAIQASKVHLLSADHEEEGEHTWRIPFDPSLKEVTISLSGPGPEIE-VRDPLG 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-MS;

A Labbe D., Garnon J., Lau P.C.K.;
Labbe D., Garnon J., Lau P.C.K.;
L. J. Bacteriol. 179:0-0(0).
EMBL: 085412; AAB52543.1; -.
InterPro; IPR000410; Bctrl_sensor.
InterPro; IPR000410; Bctrl_sensor.
InterPro; IPR000410; Bctrl_sensor.
InterPro; IPR00140; TPR.
R InterPro; IPR00140; TPR.
R Pfam: PF02518; HATPasse_c.
R Pfam: PF02518; HATPasse_c.
R SMART; SM00387; HATPasse_c.
R Pfam: PF03819; HATPasse_c.
R Pfam: PF02518; HATPasse_c.
R Pf02518; HATPas
SEQUENCE FROM N.A.
RP RC RA DR RW KW
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Search completed: March 7, 2002, 22:07:47 Job time: 3165 sec

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(without alignments)
103.136 Million cell updates/sec
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1 QVIDGASRILERSLSSRSRV.....RELRQLYVQGGGDCPEMSVG
                                                                                                                                                                                                                                                                                                                                                                                March 7, 2002, 22:05:20 ; Search time 48.12 Seconds
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| SIDS2/gcgdata/geneseq/geneseqp/AA1981.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp/AA1982.DAT:*
| SIDS2/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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| SIDS2/gcgdata/geneseq/geneseqp/AA1988.DAT:*
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   522463 segs, 74073290 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-665-728-1_COPY_56_122
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseg/genesegp/AA1998.DAT:*/SIDS2/gcgdata/geneseg/genesegp/AA1999.DAT:*/SIDS2/gcgdata/geneseg/genesegp/AA2000.DAT:*/SIDS2/gcgdata/geneseg/genesegp/AA2001.DAT:*

/SIDS2/gcgdata/geneseq/geneseqp/AA1997.DAT:*

		Description	Rat secreted facto	Sequence qi/332818	Arabidopsis thalia	Arabidopsis thalia	Human polypeptide	Human interleukin-	Mouse interleukin-	Human cardiofrophi	Human neurotrophic	Mouse neurotrophic	Amino acid sequenc
SUMMARIES		ID	AAB83147	AAY53667	AAG52665	AAG52664	AAM41239	AAB19586	AAB19587	AAE00828	AAW29715	AAW29716	AAW56141
		DB	22	21	21	21	22	21	21	22	19	19	13
	* Query	Length	275	3117	190	229	201	215	215	223	225	225	225
•	* Query	Match	100.0	51.2	18.7	18.7	18.6	18.4	18.4	18.4	18.4	18.4	18.4
		Score	342	175	64	64	63.5	63	63	63	63	63	. 63
	Result	No.	1	7	m	4	2	9	7	œ	6	10	11

cid se ardiot NT-1 p	Murine NNT-1 prote Amino acid sequenc Human protein sequ	Human lung tumour Human lung tumour	Zea mays protein f	dops	Zea mays procein i	oidops	is	Zea mays protein f	818	ß	ß	Zea mays protein f	Mouse FCTR4 protei	A multifunctional	A multifunctional	Mouse growth facto	Mouse FCTR3 protei	Human VEGF-G prote	Human protein segu	Zea mays protein f	mays	mays	late d	Breast and ovarian	Human polypeptide	Human polypeptide	Zea mays MAP kinas
AAW56142 AAW94466 AAY87813	AAY8/814 AAG63543 AAM25831	AAY29512 AAB44461	AAG26109	AAG35542	AAG40812	AAG35541	AAG14557	AAG40739	AAG34742	AAG34741	AAG14556	AAG40738	AAU00701	AAY02097	AAY02098	AAB48663	AAU00700	AAB60895	AAB94895	AAG25892	AAG41201	AAG35960	AAP94763	AAB59010	AAM39590	AAM41376	AAY44927
19 20 21	22	20	21	21	212	21	21	21	21	21	21	21	22	20	20	21	22	22	22	21	21	21	10	21	22	22	21
225 225 225	225 255 253	746	125	143	165	173	212	214	216	244	252	257	261	274	274	370	370	370	442	113	93	248	362	417	501	516	661
18.4 18.4 18.4		۲.۲	7.	۲.		7.	7.	7	•	7	7	7	7	7	7	•	7	7	7	7		7	è.	ė.	٠.	ė.	16.7
6333	939	61 61	09	09	09	9	09	09	09	9	09	9	09	09	9	09	9	9	59.5	59	28	Ŋ	57.5	57	57	57	27
12 13 14	16 16 17	18 19	20	21	23.	24	25	56	27	28	29	30	31	32	33	. 34	35	36	37	38	39			42	43	44	45

ALIGNMENTS

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Rat; secreted factor; P00210D09; cardiant; nephrotropic; antlinflammatory; gene therapy; cardiac disease; renal disease; inflammatory disease.
                                                                        Rat secreted factor encoded by clone P00210D09.
                                                                                                                                                                                7. hote-"Rat secreted factor" 35..55 /label= Transmembrane_domain /133..143 /label= Transmembrane_domain
                                                                                                                                                          1..21
/label= Signal_peptide
22..275
                                                                                                                                               Location/Qualifiers
                  AAB83147 standard; protein; 275 AA.
                                                                                                                                                                                                                                                                                             99US-0156277.
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                                                      (first entry)
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                                                     29-JUN-2001
                                                                                                                                                                                                                                                         05-APR-2001.
                                                                                                                            Rattus sp.
                                    AAB83147;
                                                                                                                                               Key
Peptide
                                                                                                                                                                          Protein
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         AAB83147
RESULT
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AAG52665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mecnanical stress; gene therapy; protein 608; osteoporosis; bone density;
bone development; g1/3328186.
                                                                      Novel secreted factor encoded by clone P00210D09 useful for diagnosing, treating and/or preventing various cardiac, renal and inflammatory
                                                                                                                                 The present sequence is a novel secreted factor encoded by rat cDNA clone P00210D09. The invention relates to a polypeptide comprising a sequence of at least 80% identity to residues 22-122 of the present sequence, or a sequence encoded by a nucleic acid hybridising under stringent conditions to the complement of the coding region comprising 1031 nucleotides, and having at least one biological activity of the polypeptide encoded by clone P00210D09. The polypeptides and polynucleotides of the invention are useful for the treatment of cardiac, renal and inflammatory diseases. The polynucleotides are useful in antisense mediated gene inhibition and in gene therapy. The polypeptides are useful in assays for identifying lead compounds that may be used as therapeutic agents in the treatment of cardiac,
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence gi/3328186 from an alignment with protein 608.
                                                                                                                                                                                                                                                                                                                  100.0%; Score 342; DB 22; 100.0%; Pred. No. 1.5e-38;
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                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY53667 standard; Protein; 3117 AA.
                                                                                                                                                                                                                                                                or inflammatory diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Einat P, Mor O, Skaliter R,
                                                                                                                Claim 9; Fig 1; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0085673.
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                                                                                                                                                                                                                                                                                                                                     Conservative
                    Stanton LW, Kapoun AM;
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                                       WPI; 2001-328177/34
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 67; Conserv
                                                                                                                                                                                                                                                                                    275 AA;
(SCIO-) SCIOS INC.
                                                  N-PSDB; AAF82464
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY53667;
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                                                                                             diseases
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The present sequence is obtained from a clustral X alignment with protein 608. Protein 608 was identified using the method of the invention after subjecting rat osteoblasts to mechanical stress. Expression of the 608 gene was found to be uprequiated by about 3-fold in cells subjected to mechanical strain. The specification describes a method for the cells of genes responsive to a specific mechanical stress. The method comprises applying the mechanical stress to an organism (tissue correctls comprising bone cells), isolating the specific cellular correctls comprising bone cells), isolating the specific cellular cannow in comparison with control samples. The method is used to identify genes whose expression is responsive to a specific stress. The identified comprises state. The risk determination methods are used for teasting a medicament for gene therapy. These medicaments, or genes identified by the method of the invention, are used for treating, preventing or controlling a physiological or disease state (especially osteoporosis or bone density or other factors causing or contributing to osteoporosis or its symptoms or other conditions involved in mechanical stress or its lack. The methods can also be used for advancing research or studies in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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preventing, treating or controlling osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.2%; Score 175; DB 21;
ilarity 45.5%; Pred. No. 2.2e-14;
Conservative 16; Mismatches 20;
                                                                Claim 32; Fig 6A-R; 308pp; English.
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Matches 30; Conserv
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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06-APR-1999;
08-APR-1999;
16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                       5; Mismatches 17; Indels
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                                                                                                                                                                                                                                                                                                          18.7%; Score 64;
42.9%; Pred. No. ]
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990S-0159330.
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990S-0159638.
990S-0159638.
990S-0160741.
990S-0160770.
990S-0160770.
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Matches 21; Conservative
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14-0CT-1999;
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26-0CT-1999;
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01-APR-1999
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99US-0147416
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21-OCT-1999;
21-OCT-1999;
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2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang D;
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Zhang J;
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                                                                                                                                                                                  Length 229
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Pred. No. 1.3;
.5; Mismatches 17; Indels
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Yang Y,
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Wang J, Wang Z, Wehrman T, Xu C, Xue AJ,
Zhao QA, Zhou P, Goodrich R, Drmanac RT;
                                                                                                                                                                                                                                                                                                 AAM41239 standard; Protein; 201 AA
                                                                                                                                                                                                                                                                                                                                                            Human polypeptide SEQ ID NO 6170.
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2000US-055317.
2000US-0598042.
2000US-0653450.
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2000US-0653450.
2000US-0653450.
990S-0160768.
990S-0160710.
990S-0160814.
990S-0160818.
990S-0160980.
990S-0160981.
990S-0161404.
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42.9%;
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                                                                                                                                                                                                       Conservative
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Best Local Similarity
Matches 21; Conserv
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14-SEP-2000;
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09-JUL-2000;
19-JUL-2000;
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21-0CT-1999;
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The present sequence is that of human interleukin-B60 (IL-B60), a novel, small soluble cytokine-like protein that exhibits structural motifs characteristic of a member of the long-chain cytokines, and motifs characteristic of a member of the long-chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-60B may have either stimulatory or inhibitory ceffects on haematopotetic cells, including e.g. lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, character cells, haematopotetic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or tissue culture cells by contexting the cell with an agonist or antagonist of IL-B60 or an agonist of antagonist of a complex of mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see CABB19588). The IL-B60/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. IL-60B, its autolmmune disorders and also for drug screening.
                polypeptides, and nucleic acids, useful in research, diagnosis and for treating inflammatory and autoimmune disorders -
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haematopoietic; inflammation; antiinflammatory; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%; Score 63; DB 21;
38.9%; Pred. No. 1.6;
ive 5; Mismatches 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :| || | | : || | |:|| | |:|| | |:|| | |:|| | |:|| | |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:|| |:||
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18..215
/label- Mature-protein
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                                                                                                      Claim 1; Page 15-16; 97pp; English.
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Matches 14; Conservative
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N-PSDB; AAA88547.
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                                                                                   the encoded polypeptides (AMM421313) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, and thrombolytic activity, chemotactic/chemokinetic activity, haemostatic assays for receptor activity, arthritis and inflammation, leukaemias and CNNS disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note: The sequence data for this patent did not form part of the printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human nucleic acids (AAIS7798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LERSLSSRSRVIANYALVPF------HDPDIGPVTLTADPVVFQRELRQLYVQGGGD-- 60
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haematopoietic; inflammation; antiinflammatory; autoimmune disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
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Pred. No. 1.3;
16; Mismatches 21;
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SEQ ID NO 6170; 10078pp; English.
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/label= Signal_peptide
18..215
/label= Mature-protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18.6%;
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Best Local Similarity 27.5%
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SCHE ) SCHERING CORP.
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N-PSDB; AAA88546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 201 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ---CPEMSV 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
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Example 2;
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Peptide
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                             AAW29715;
                                                                                                                                                                                   Sequence
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                                             The present sequence is that of mouse interleukin-B60 (IL-B60), a novel, small soluble cytokine-like protein that exhibits structural motifs characteristic of a member of the long-chain cytokines, and which shows homology to granulocyte colony stimulating factor and interleukin-6. IL-60B may have either stimulatory or inhibitory caffects on haematopoietic cells, including e.g. lymphoid cells, such as T-cells, B-cells, natural killer cells, macrophages, dendritic cells, haematopoietic progenitors, etc. Methods are provided for modulating the physiology or development of a cell or tissue culture cells by contacting the cell with an agonist of antagonist of IL-B60 or an agonist of antagonist of a complex of mature IL-B60 and its partner, cytokine-like factor-1 (CLF-1, see CRAB19588). The IL-B60/CLF-1 cytokine serves as a key physiological factor in motor neuron development and regeneration. IL-60B, its autoimmune disorders and also for drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; biologically active complex; haemopoietin receptor; NR6;
cardiotrophin-like cytokine; CLC; therapy; prophylaxis; proliferation;
differentiation; cell survival; neurotrophic activity.
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                                                                                                                                                                                                                                                                                                               Score 63; DB 21; Length 215; Pred. No. 1.6;
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/label= Signal_peptide
/label= Human_mature_CLC_protein
/note= "Cardiotrophin-like cytokine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cardiotrophin-like cytokine (CLC) protein.
treating inflammatory and autoimmune disorders
                                                                                                                                                                                                                                                                                                                                                                                  7 SRILERSLSSRSRVIANYALVPFHDPDIGPVTLTAD 42
                                                                                                                                                                                                                                                                                                                                          5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAE00828 standard; Protein; 223
                        Claim 1; Page 17; 97pp; English
                                                                                                                                                                                                                                                                                                                18.4%;
38.9%;
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                                                                                                                                                                                                                                                                                                                                          14; Conservative
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, Hasegawa M;
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N-PSDB; AAD04201.
                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                           AA;
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                                                                                                                                                                                                                                                                                                                Query Match
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Matches
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The present invention relates to a biologically active complex comprising a haemoplotein receptor, NKG and cardiotrophin-like cytokine (CLC). The complex is useful in the manufacture of a medicament for the treatment and/or prophylaxis of a subject, as it is involved in facilitating proliferation, differentiation and/or survival of a cell. The complex or its components have neurotrophic activity. The present sequence is human cardiotrophin-like cytokine (CLC) protein.
                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Newly isolated nucleic acid encoding human or murine neurotrophic factor NNT-1 - useful for treatment of neurological and immunological diseases or inflammation, also as vaccine adjuvant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NNT-1; neurotrophic factor; human; antiinflammatory; adjuvant; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; peripheral neurophathy; dystrophy; neural retina degeneration; common variable immunodeficiency; CVID; selective IgA deficiency; hypogammaglobulinaemia; X-linked agammaglobulinaemia; antiseptic;
                                                                                                                                                                                                                                                                                                                                     ö
New biologically active complex comprising NR6 and cardiotrophin-like-cytokine, for facilitating proliferation, differentiation and/or survival of a cell -
                                                                                                                                                                                                                                                                                                 Length 223;
                                                                                                                                                                                                                                                                                      Score 63; DB 22; Length 22
Pred. No. 1.7;
Vismatches 17; Indels
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                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    7 SRILERSLSSRSRVIANYALVPFHDPDIGPVTLTAD
                                                                     Claim 32; Page 114-115; 123pp; English
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/label= Sig_peptide
28..225
/label= Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human neurotrophic factor NNT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW29715 standard; Protein; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 3; 120pp; English
                                                                                                                                                                                                                                                                                                  18.4%;
38.9%;
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 14; Conserv
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                                                                                                                                                                                                                                               223 AA;
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This is the amino acid sequence of a novel neurotrophic factor, designated NNT-1, that is a growth factor for neurons and for B or T cells. It was deduced from isolated CDNA (see AAV4751) and genomic DNA (see AAV4751) clones. Vectors containing the cDNA or genomic DNA and host cells are provided for use in the production of NNT-1 polypeptides. These are used to treat: (i) neurological or immunological diseases, specifically Alzheimer's, Parkinson's or Huntington's diseases, smyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, peripheral neuropathy, dystrophy and degeneration of the neural retina, or conditions characterised by T or B cell defects, eg. common variable immunodeficiency (CVID), selective IgA deficiency, hypogammaglobulinaemia and X-linked and malamation. NNT-1 is also able to boost immunoreactivity and antibody production following vaccination, and, since it inhibits treating sepsis. In addition, cells that have been engineered to express NNT-1 can be implanted, or nucleic acids are delivered in gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NNT-1; neurotrophic factor; mouse; antiinflammatory; adjuvant; Alzheimer's disease; Parkinson's disease; Huntington's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; peripheral neurophathy; dystrophy; neural retina degeneration; common variable immunodeficiency; CVID; selective IgA deficiency; hypogammaglobulinaemia; x-linked agammaglobulinaemia; antiseptic;
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                                                                                                                                                                                                                                                                                                                                                                                      DB 19; Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                7 SRILERSLSSRSRVIANYALVPFHDPDIGPVTLTAD 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              47 trylehqirslagtylnylgppfnepdfnpprigae 82
                                                                                                                                                                                                                                                                                                                                                                                      Score 63; DB 1
Pred. No. 1.7;
5; Mismatches
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28..225
/label- Mat_protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW29716 standard; Protein; 225 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse neurotrophic factor NNT-1.
                                                                                                                                                                                                                                                                                                                                                                                    18.4%;
38.9%;
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97US-0792019
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Best Local Similarity 38.9°
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                      225 AA;
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                                                                                                                                                                                                                                                                                                                                      Sequence
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ID AAW2
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This is the amino acid sequence of a murine neurotrophic factor, designated NNT-1, that is a growth factor for neurons and for B or T cells. It was deduced from isolated NNT-1 (See AAV47512).

Human NNT-1 (see AAV47915) is also provided. Vectors and host cells for use in the production of human murine recombinant NNT-1 (See AAV47915).

Con use in the production of human murine recombinant NNT-1 (See AAV47915) is also provided. Vectors and host cells for use in the production of human murine recombinant NNT-1 (Innunclogical diseases, specifically Alzheimer's, Parkinson's or Huntington's diseases, amyotrophic lateral sclerosis, charcotro-warie-rooth syndrome, peripheral neuropathy, destrophy and degeneration of the neural retina, or conditions characterised by T or B cell defects, e.g. common variable immunodeficiancy (CVID), caselective IgA deficiency, hypogammaglobulinaemia and X-linked agammaglobulinaemia (claimed) but many others disclosed; and (11) inflammation. NNT-1 is also able to boost immunoractivity and antibody production following vaccination, and, since it inhibits treating sepsis. In addition, cells that have been engineered to express NNT-1 can be implanted, or nucleic acids are delivered in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron; treatment; neurological disease; degeneration; Parkinson's disease; amyotropic lateral sclerosis; ALS; Alzheimers's disease; stroke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                               Newly isolated nucleic acid encoding human or murine neurotrophic factor NNT-1 - useful for treatment of neurological and immunological diseases or inflammation, also as vaccine adjuvant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of human neurotrophic factor NNT-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 63; DB 19;
Pred. No. 1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 SRILERSLSSRSRVIANYALVPFHDPDIGPVTLTAD 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "signal peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                        Claim 13; Fig 5; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.4%;
38.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 38.9
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene therapy vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          225 AA;
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N-PSDB; AAV47512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAW56141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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Gaps

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neurons. The NNT-1 protein is useful in the treatment of neurological diseases characterised by the degeneration and death of particular classes of neurons. These diseases specifically include Parkinson's disease, amyotropic lateral sclerosis (ALS), Alzheimers's disease, stroke and various degenerative disorders affecting vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a novel cardiotrophin-like cytokine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated cardiotrophin-like cytokine nucleic acid - used to develop products for treating cardiac and immune system disorders, e.g. heart failure, hypertension, cancers, autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; cardiotrophin-like cytokine; interleukin 6 cytokine family; CLC; IL-6; diagnosis; detection; immune system-related disorder; cancer; cardiac disorder; heart failure; hypertension; cancer; autoimmune disorder; infection.
                                                                                                                                                                                       ö
                                                                                                                                                     Length 225;
                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label- Cardiotrophin-like_cytokine
                                                                                                                                                                                       17;
                                                                                                                                                   Score 63; DB 19;
Pred. No. 1.7;
                                                                                                                                                                                                                                               7 SRILERSLSSRSRVIANYALVPFHDPDIGPVTLTAD 42
                                                                                                                                                                                       5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cardiotrophin-like cytokine protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "conserved domain"
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/note= "conserved domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "conserved domain"
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                                                                                                                                                                                                                                                                                                                                           AAW94466 standard; Protein; 225
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/label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= CD-III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                       18.4%;
38.9%;
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                                                                                                                                                                                        Conservative
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                                                                                                                                                                       Local Similarity
                                                                                                       225 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections
                                                                                                                                                                                          14;
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                                                                                                                                                                                                                                                                                                                                                                            AAW94466;
                                                                                                       Sequence
                                                                                                                                                         Query Match
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Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a murine neurotrophic factor, designated NNT-1, which is capable of stimulating growth of motor or sympathetic
                                                                                                                                                     The present sequence represents a human neurotrophic factor, designated NNT-1, which is capable of stimulating growth of motor or sympathetic neurons. The NNT-1 protein is useful in the treatment of neurological diseases characterised by the degeneration and death of particular classes of neurons. These diseases specifically include Parkinson's disease, amyotropic lateral sclerosis (ALS), Alzheimers's disease, stroke and various degenerative disorders affecting vision.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse; neurotrophic factor; NNT-1; growth; motor; sympathetic; neuron; treatment; neurological disease; degeneration; Parkinson's disease; amyotropic lateral sclerosis; ALS; Alzheimers's disease; stroke.
                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neurotrophic factor NNT-1 polypeptide and related nucleic acids useful for stimulating growth of motor and sympathetic neurons
                                                                        ophic factor NNT-1 polypeptide and related nucleic acids for stimulating growth of motor and sympathetic neurons
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                                                                                                                                                                                                                                                                                                                                            Length 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid sequence of murine neurotrophic factor NNT-1.
                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                DB 19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 :| || || : || || || || || || || 47 trylehqlrslagtylnylgppfnepdfnpprlgae 82
                                                                                                                                                                                                                                                                                                                                            Score 63; DB 1
Pred. No. 1.7;
5; Mismatches
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/note= "mature peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 5; 41pp; English.
                                                                                                                           Claim 1; Fig 3; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                18.4%;
38.9%;
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                                                                                                                                                                                                                                                                                                                                                              Local Similarity 38.9
nes 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1998-260526/23.
                      WPI; 1998-260526/23.
N-PSDB; AAV22652.
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                                                                                                                                                                                                                                                                                               225 AA;
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                                                                         Neurotrophic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US5741772-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNT-1; human; neurotrophic factor; nootropic; neuroprotective; treatment; anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological; nervous system degeneration; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; Huntington's disease; peripheral neuropathy; neural retina degeneration; retinopathy; immune disorder; hematopoietic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acids encoding neurotrophic factors useful for stimulating growth of motor or sympathetic neurons for treating neuron cell damage
(CLC) protein which is a member of the interleukin 6 (IL-6) cytokine family. The present sequence represents the human CLC protein. The present invention also describes screening methods for identifying
                                                                                                                                                                                                                                                                      Gaps
                                                   agonists and antagonists of CLC activity, as well as methods for detecting cardiac and immune system-related disorders and therapeutic methods for treating cardiac and immune system-related disorders, e.g heart failure, hypertension, cancers, autoimmune disorders and infections.
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                                                                                                                                                                                                                              DB 20; Length 225;
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                                                                                                                                                                                                                                                                17;
                                                                                                                                                                                                                                                                                           7 SRILERSLSSRSRVIANYALVPFHDPDIGPVTLTAD 42
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                                                                                                                                                                                                                        18.4%; Score 63; DB 38.9%; Pred. No. 1.7; Live 5; Mismatches
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                                                                                                                                                                                                                                                          14; Conservative
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                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 14; Conserv
                                                                                                                                                                  225 AA;
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                                                                                                                                                                    Sequence
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as retinitis pigmentosa, drug-induced retinopathies, stationary forms of hematopoietic disorders. (I) is effective in treating neurological conditions and promotes neuron regeneration. Immune disorders and conditions and promotes neuron regeneration. Neural functions are effectively restored in patients suffering from various neurological disorders. This sequence represents the human NNT-1 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a novel nucleic acid molecule (I) encoding a novel neurotrophic factor (NNT-1) (II) which has nootropic, neuroprotective, anticonvolusant, antiparkinsonian, antidabetic and ophthalmological activity. (I) is useful for producing NNT-1 polypeptides which are useful for treating patients in whom various cells of the central, autonomic, or peripheral nervous system have degenerated and/or have been damaged by congenital disease, trauma, mechanical damage, surgery, stroke, ischemia, infection, metabolic disease, nutitional deficiency, malignancy and/or toxic agents. NNT-1 proteins are used to treat diseases like Alzheimer's, parkinson's, amyotrophic lateral sclerosis, Charcot-Marie-Tooth syndrome, Huntington's disease, peripheral neuropathy induced by diabetes or other metabolic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NNT-1; neurotrophic factor; nootropic; neuroprotective; treatment; anticonvulsant; antiparkinsonian; antidiabetic; ophthalmological; nervous system degeneration; Alzheimer's disease; Parkinson's disease; amyotrophic lateral sclerosis; Charcot-Marie-Tooth syndrome; murine; Huntington's disease; peripheral neuropathy; neural retina degeneration; retinopathy; immune disorder; hematopoietic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acids encoding neurotrophic factors useful for stimulating growth of motor or sympathetic neurons for treating neuron cell damage
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         retina
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 and/or dystrophies or degeneration of the neural
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                                                                                                                                                                                                                                                                                          7 SRILERSLSSRSRVIANYALVPFHDPDIGPVTLTAD 42
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                                                                                                                                                                                                                        ; DB 2
                                                                                                                                                                                                                                                           5; Mismatches
                                                                                                                                                                                                                        Score 63;
Pred. No. 1
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                                                                                                                                                                                                                     18.4%;
38.9%;
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                                                                                                                                                                                                                                                         14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Murine NNT-1 protein.
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N-PSDB; AAA39483.
                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                225 AA;
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                                                                                                                                                                  Seguence
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disorders, and/or dystrophies or degeneration of the neural retina such as retinits pigmentosa, drug-induced retinopathies, stationary forms of night blindness, progressive cone-rod degeneration, immune disorders and hematopoietic disorders. (I) is effective in treating neurological conditions and promotes neuron regeneration. Neural functions are effectively restored in patients suffering from various neurological disorders. This sequence represents the murine NNT-1 protein described in the method of the invention.
   8888888888
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225 AA; Sequence

ö Gaps ö Query Match 18.4%; Score 63; DB 21; Length 225; Best Local Similarity 38.9%; Pred. No. 1.7; Matches 14; Conservative 5; Mismatches 17; Indels

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Search completed: March 7, 2002, 22:05:21 Job time: 4639 sec

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OM protein - protein search, using sw model

Run on: March 7, 2002, 22:06:20 ; Search time 36.48 Seconds

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139.904 Million cell updates/sec

Title: US-09-665-728-1_COPY_56_122
Perfect score: 342
Sequence: 1 QVIDGASRILERSLSSRSRV......RELRQLYVQGGGDCPEMSVG
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

67

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_68:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	_	P-qlycoprotein hom	probable ABC trans	Cal	-0			0	P-qlycoprotein-lik	probable P-glycopr			inordanic pyrophos	protein T25K16.5	transcription requ	inordanic ovrophos	probable fattv-aci	light harvesting c	ທ	hypothetical prote	>		Ω			-	_	П
SUMMARIES	ΩI	T20992	T43290	T48007	T02187	S59316	R5DO2	A27131	GQFFE	D85023	T52319	E85023	D70929	T07594	T01946	C86141	F69716	T01370	E69438	S51658	B48067	B85436	T43405	S75270	D49348	C83719	T50971	T47174	T30382	34
	DB	7	7	7	ď	~	Н	7	Н	~	7	7	7	~	7	7	~	7	7	7	~	~	7	7	7	~	7	~	~	~
	Length	5175	5198	1292	1286	269	237	843	1330	1229	1229	1230	67	211	216	230	178	214	552	275	323	415	512	237	342	380	114	283	359	399
dР	Query Match			•					œ,	œ.	•	•		٠	•	•	•	•	•	17.1	•		•		17.0	•	9	16.7	16.7	16.7
	Score	175	175	71.5	70.5		(7)	62.5	(7	62	62		60.5	9	9		59.5	59	59	58.5	œ.	∞ .	œ	28	28	28	57	57	57	22
	Result No.	-	7	m	4	S	9	7	æ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	52	56	27	28	58

RESULT 2
T43290
T63291
T63290
T6. Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Species: T43290; Esquence_revision 11-Jan-2000 #text_change 18-Feb-2000
C; Accession: T43290; T2993; T24734
R; Vogel, B.E.; Hedgecock, E.M.

61 CPEMSV 66 ||| :: 113 CPEKTL 118

Qy Db

ribonucleoside-dip	membrane transport	probable recB prot	probable multi-dom	probable signal pe	hypothetical prote	hypothetical prote	conserved hypothet	probable ABC trans	glutamate synthase	MAP kinase (EC 2.7	cell division cvcl	protein kinase (EC	probable fadA5 pro	glutathione reduct	hypothetical prote
G69457	T40296	C70612	T37056	B83484	A70759	G85434	C69991	F86155	C75551	S53536	149066	S52419	C70677	A64052	B36793
7	7	~	~	7	7	7	~	7	7	7	~	N	~	~	N
752	580	1094	2082	179	285	344	428	1229	1615	360	360	360	391	456	1434
16.7	16.5	16.5	16.5	16.4	16.4	16.4	16.4	16.4	16.4	16.2	16.2	16.2	16.2	16.2	16.2
57	56.5	56.5	56.5	26	26	26	26	26	26	55.5	55.5	55.5	55.5	55.5	55.5
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 T20992		
hypothetical protein F15G9.4a - C	hypothetical protein F15G9.4a - Caenorhabditis elegans C. Speries: Caenorhabditis elegans	
C; Date: 15-Oct-1999 C: Accession: T20992:	C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000 C.Accession: 720992: 724733	0
R; Sulston, J.		
submitted to the EMB	submitted to the EMBL Data Library, December 1994	
A; Reference number: 7 A; Accession: T20992	9355	
A; Status: preliminary	A; Status: preliminary; translated from GB/EMBL/DDBJ	
A; Molecule type: DNA		
A; Residues: I-51/5 <wil> A:Cross-references: EMBI</wil>	A):Kesidues; 1-51/5 (WILL) A):Kesidues; Engl. 3/70Kg; BIDN: 7/10Kg; 1: Cenp. 7/10Kg; Geo.	4
A; Experimental source: clone F15G9	clone F1569	Q
R; Kershaw, J.		
submitted to the EMB	submitted to the EMBL Data Library, December 1994	
A; Reference number:	9929	
A; Accession: T24/33	A;ACCESSION: 124/33 A.Status: orealiminary: translated from CD/DND1	
A; Molecule type: DNA		
A; Residues: 1-5175 <wi2></wi2>	2>	
A;Cross-references: 1	A; Cross-references: EMBL: 247070; PIDN: CAA87344.1; GSPDB: GN00028; CESP: F15G9.4a	9.4a
A, Experimental source: clone T09B9	clone T09B9	
C;Genetics:		
A; Gene: CESP:F15G9.4a		
A; Map position: X		
A; Introns: 85/1; 120,	A; Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3;	051/3;
2512/2; 2593/3; 26	/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2	2991/3;
1; 4225/1; 4361/1; 44	8/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1;	5011/1
Query Match	51.2%; Score 175; DB 2; Length 5175;	
Matches 30; Cons	30; Conservative 16; Mismatches 20; Indels 0; Gaps	0;
Qy 1 QVIDGASRILE	1 QVIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGD 60	
: :: :		
50	VMAQKEKLIYNYIMVPFHDPYLGELINTTDSTYFMKQLSKvrvhGGGD 112	

ä

Indels

23;

Pred. No. 1.6;); Mismatches

10;

29.18;

...-TADPVVFQR 48 23;

9 ILERSLSSRSRVIANYALVPFHDPDIGPVTL-----

49 ELRQLYVQG-GGDCPEMSV 66

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probable ABC transporter [imported] - Arabidopsis thaliana
N.Alternate names: hypothetical protein F14M4.17
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: D. Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M submitted to the EMBL Data Library, September 1998
A. Reference number: 214609
A. Reference number: 214609
A. Reference number: 214609
A. Residuas: Lranslated from GB/EMBL/DDBJ
A. Status: translated from GB/EMBL/DDBJ
A. Residuas: 1-1266 AROU>
A. Residuare 402, 761-768, 1999
A. Residuare 402, 761-768, 1999
A. Residuare and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A. Reference number: A. Residuary
A. Molecula type: DNA
A. Molecula type: DNA
                                                                                                                                                                                                                                1139 TIRANIAYGKGGDATETEI 1157
                    Best Local Similarity 29.1
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              859316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: him-4; F15G9.4b
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-glycoprotein homolog T17J13.110 [similarity] - Arabidopsis thaliana
N.Alternate names: protein T17J13.110
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Sacession: T48007
C.Accession: T48007
C.Accession: T48007
A.Reference number: 224482
A.Accession: T4807
A.Coostreferences: EMBL:Al.138651
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ-
A;Reference number: 222396
A;Accession: T43290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Map position: 3
A:Introns: 123/3: 142/1; 200/3: 354/2; 529/3; 621/1; 904/3; 989/3; 1077/3; 1175/3
A:Introns: 123/3: 142/1; 200/3: 354/2; 529/3; 621/1; 904/3; 989/3; 1077/3; 1175/3
A:Note: T1713.110
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
E;421-615/Domain: ATP-binding cassette homology <ABC1>
F;1066-1261/Domain: ATP-binding cassette homology <ABC2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-5198 <WIL>
Cross-references: BrBL:247068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
Experimental source: clone F1569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
Residues: 1-5198 <WIZ-S
Cross-references: EMBL:247070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
Experimental source: clone T0989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51.2%; Score 175; DB 2; L
ilarity 45.5%; Pred. No. 7.8e-13;
Conservative 16; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reslouce.
A; Cross-references: Erro...
A; Experimental source: clone F15Gy
A; Experimental source: clone F15Gy
B; Kershaw, J.
Submitted to the EMBL Data Library, December 1994
A; Reference number: 219929
A; Reference number: 219929
A; Recession: T24734
A; Crossion: T24734
A; Crossio
                                                                                                                                                                                                                      Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                     Molecule type: mRNA
Residues: 1-5198 <VOG>
Cross-references: EMBL:AF074901; PIDN:AAC26792.1
                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CPEKTL 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CPEMSV 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
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A; Map position: 2
A; Map position: 2
A; Introns: 104/3; 123/1; 181/3; 255/3; 335/2; 602/1; 894/3; 983/3; 1071/3; 1169/3
A; Introns: 104/3; 123/1; 181/3; 255/3; 335/2; 602/1; 894/3; 983/3; 1071/3; 1169/3
C; Superfamily: multidrug resistance protein; ATP-binding cassette homology cABCl>
F; 1060-1255/Domain: ATP-binding cassette homology cABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein YLR128w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L3111
(Species: Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence_revisiae
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 29-Oct-1999
C;Accession: S59316; S64965; S64970; S69415
R;Delius, H.
submitted to the EMBL Data Library, June 1995
A;Description: 36.8 kb of S.cerevisiae chromosome XII including ACE2, CKI1, PDC5, A;Reference number: S59313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ä
A;Molecule type: DNA
A;Residues: 1-1286 <STO>
A;Cross-references: GB:AE002093; NID:g3522943; PIDN:AAC34225.1; GSPDB:GN00139
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----TADPVVFQR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                             Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Indels
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 20.6%; Score 70.5; DB 2; Best Local Similarity 27.8%; Pred. No. 2.1; Matches 22; Conservative 11; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 ILERSLSSRSRVIANYALVPFHDPDIGPVTL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 ELRQLYVQG-GGDCPEMSV 66
                                                                                                                                     A; Gene: F14M4.17; At2g47000
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DB 2; Length 1292;

20.9%; Score 71.5;

Query Match

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Lawred Blanch of the

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Cincossion: A00640; A38021
R:Livneh, E.; Glazer, L.; Segal, D.; Schlessinger, J.; Shilo, B.Z.
Cell 40, 599-607, 1985
A;Title: The Drosophila EGF receptor gene homolog: conservation of both hormone b A;Title: The Drosophila EGF receptor A;Title: The A;Molecule type: DNA A;Reference number: A00640; MUD:85124611
A;Molecule type: DNA A;Residues: 1-1330 <LIV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:K03054
R;Wadsworth, S.C.; Vincent III, W.S.; Bilodeau-Wentworth, D.
Rature 314, 178-180, 1985
A;Title: A Drosophila genomic sequence with homology to human epidermal growth factories number: A38021; MUID:85137938
A;Accession: A38021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 'A', 832-866, 'V', 868-943, 'QTPSLVK' <WAD>
A; Residues: 'A', 832-866, 'V', 868-943, 'QTPSLVK' <WAD>
A; Residues: 'A', 832-866, 'V', 868-943, 'QTPSLVK' <WAD>
A; Cross-references: EMBL:X02293; NID:97922; PIDN:CAA26157.1; PID:9929565
C; Comment: This sequence is tentative because the introns have not been identified C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics: A; Genetics: Flybase: Flyba
                                                                                                                                                                                                                                                                                                                                              epidermal growth factor receptor - fruit fly (Drosophila melanogaster) (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                          C; Species: Drosophila melanogaster
C; Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 23-May-1997
C; Accession: A27131
R; Schejter E.D.; Segal, D.; Glazer, L.; Shilo, B.Z.
Cell 46, 1091-1101, 1986
A; Title: Alternative 5' exons and tissue-specific expression of the Drosophila A; Reference number: A27131; MUID:87002474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidermal growth factor receptor - fruit fly (Drosophila melanogaster)
N;Contains: protein-Tyrosine kinase (EC 2.7.1.112) erbB
C;Species: Drosophila melanogaster
C;Species: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Cross-references: FlyBase:FBgn0003731
C;Superfamily: epidermal growth factor receptor; protein kinase homology
C;Keywords: ATP; growth factor receptor
                                                                         --- YVQGGG--DCPEMSVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   373 VIDGNIRILDQTFSGFQDVANYTM-----GPRYIPLDP----ERREVF 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 VIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLY 54
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                   SRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQL --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A27131
A; Molecule type: mRNA
A; Residues: 1-843 <SCH>
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: FlyBase:Egfr
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A; Accession: $59316
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Forest references: EMBL:X91258; NID:9995686; PIDN:CAA62639.1; PID:9995690
A; Cross-references: Exrain $288C
A; Experimental source: strain $288C
A; Werhasselt, P.; Voet, M.; Volckaert, G.
Submitted to the Protein Sequence Database, May 1996
A; Reference number: $64943
A; Accession: $64965
A; Reference number: $64965
A; Residues: 1-269 < VERS
A; Cross-references: EMBL:Z73300; NID:91360536; PIDN:CAA97697.1; PID:e245567; PID:9136053
A; Experimental source: strain $288C
B; Delius, H.; Hebling, U.
B; Delius, H.; Hebling, U.
B; Delius, B; A; Reference number: $64967
A; Reference number: $6
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C; Species: Dictyostellum discoideum
C; Species: Dictyostellum discoideum
C; Species: Dictyostellum discoideum
C; Species: Dictyostellum discoideum
C; Accession: S06087
R; Singleton, C.K.
Nucleic Acids Res. 17, 7989, 1989
A; Rieference number: S06087; MUID:90016885
A; Recession: S06087
A; Reference number: S06087; MUID:90016885
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:273300; NID:g1360536; PIDN:CAA97697.1; PID:e245567; PID:g136053
A;Experimental source: strain S288C
R;Verhasselt, P.; Volckaert, G.
submitted to the EMBL Data Library, September 1995
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A; Residues: 1-237 <SIN>
A; Residues: 1-237 <SIN>
A; Residues: 1-237 <SIN>
A; Residues: 1-237 <SIN>
A; Cross-references: EMBL: X15710; NID:g7354; PIDN:CAA33741.1; PID:g7355
A; Note: the authors translated the codon CAC for residues 22 and 23 as Gly and TTC for R; Singleton, C.K.; Delude, R.L.; McPherson, C.E.
Bc; Singleton, C.K.; Delude, R.L.; McPherson, C.E.
A; Title: Characterization of genes which are deactivated upon the onset of development A; Reference number: S09166; MUID:87106347
A; Contents: annotation; differential expression
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C;Superfamily: Escherichia coli ribosomal protein L2
C;Keywords: protein biosynthesis; ribosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
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32.7%; Pred. No. 1.6;
tive 10; Mismatches
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Best Local Similarity 36.2%;
Matches 21; Conservative (
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A; Accession: S69415
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Best Local S:
Matches 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 61; DB
; Pred. No. 32;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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: | | : | | : | 1 | 1075 TIRSNIAYGKGGDEASEAEI 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.8%;
26.2%;
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Best Local Similarity 26.2%
Matches 21; Conservative
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                 A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1230 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: AT4901830
                                                                                                                                                                                                                                                                                                                                                                                                                         A; Map position: 4
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: T52319
R; Sidler, M.; Dudler, R.
Submitted to the RNBL Data Library, December 1997
A; Reference number: Z26034
A; Accession: T52319
A; Reference number: Z26034
A; Accession: T52319
A; Refarence number: Z26034
A; Residues: T52319
A; Residues: L1229 <SID>A; Residues: L1229 <SID>A; Cross-references: EMBL:Y15990; PIDN:CAA75922.1
A; Residues: City Countries: Columbia C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Introns: 68/3; 86/3; 145/3; 219/3; 299/3; 565/3; 836/3; 925/3; 1013/3; 1112/3
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A;Nolecule type: DNA
A;Residues: 1-1229 <STO>
A;Cross-references: GB:NC_001268; NID:g7268566; PIDN:CAB80675.1; GSPDB:GN00140
C;Genetics:
A;Gene: Af4g01820
A;Map position: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 ILERSLSSRSRVIANYALVPFHDPDIGPVTLT-------ADPVVFQR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23; Indels 24; Gaps
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                                                                         13;
                                                                                                                                24;
                                                                                                        2 VIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLY 54
                                 Length 1330;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1229;
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                                                                       Indels
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                                                                     14;
                                 DB 1;
                             Score 62.5; DB
Pred. No. 23;
8; Mismatches
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18.1%; Score 62; DB
Best Local Similarity 26.2%; Pred. No. 24;
Matches 21; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12; Mismatches
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34.0%;
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                    Query Match
Best Local Similarity 34.09
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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Matches 21; Conserv
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T52319
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C;Accession: E85023
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488
A;Accession: E85023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probable ferredoxin - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 17-Mar-2000
C;Accession: D70929
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gord
R;Cole, S.T.; Brosch, R.; Perkhill, T.; Gentles, S.; Hamili, N.; Holroy
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Attle: Decliphering the biology of Mycobacterium tuberculosis from the complete ge
A;Accession: D70929
A;Accession: D70929
A;Accession: D70929
A;Accession: D70929
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A:Residues: 1-67 <COL>
A:Cross-references: GB:AL022021; GB:AL123456; NID:g3250699; PIDN:CAA17708.1; PID:e1
A:Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: Rv1786
C;Superfamily: unassigned ferredoxin 2[4Fe-4S]-related proteins; ferredoxin 2[4Fe-4
F;3-62/Domain: ferredoxin 2[4Fe-4S] homology <FER>
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:NC_001268; NID:97268567; PIDN:CAB80676.1; GSPDB:GN00140
C;Genetics:
probable P-glycoprotein-like protein (imported) - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 16-Feb_2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24;
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A; Gene: T25K16.5
A; Map position: 1
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probable inorganic pyrophosphatase (EC 3.6.1.1), soluble PPA - potato C.Species: Solanum tuberosum (potato) C.Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 11-May-2000 C.Accession: T07594 R.du Jardin, P.; Rojas-Beltran, J.; Gebhardt, C.; Brasseur, R. Piant Physiol. 109, 853-860, 1995 Plant Physiol. 109, 853-860, 1995 A.Title: Molecular cloning and characterization of a soluble inorganic pyrophosphatase A.Reference number: Z16037; MUID:96163189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-216 <ABU>
A;Cross-references: EMBL:AF096370; NID:q3695372; PIDN:AAC62786.1; PID:g3695383
A;Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inorganic pyrophosphatase homolog F1104.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 22-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:236894; NID:9534915; PIDN:CAA85362.1; PID:9534916
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.5%; Score 60; DB 2; Length 211; 46.3%; Pred. No. 5.1;
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A;Description: The sequence of A. thallana F1104.
A;Reference number: Z14466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Description: catalyzes the hydrolysis of pyrophosphate
C;Superfamily: inorganic pyrophosphatase
C;Keywords: hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 46/1; 55/3; 77/3; 113/3; 135/3; 176/1; 203/2
A;Note: F1104.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 APRLNERILSSISR--RSVAAHPWHDLEIGPEA----PSVF 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6 ASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVF 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 RILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-211 <DUJ>
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C;Superfamily: inorganic pyrophosphatase
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Best Local Similarity 46.35
Matches 19; Conservative
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C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzbergy, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ,
                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE005172; NID:g6715648; PIDN:AAF26475.1; GSPDB:GN00141
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.5%; Score 60; DB 2; Length 230; Best Local Similarity 51.6%; Pred. No. 5.6; Matches 16; Conservative 4; Mismatches 9; Indels
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                                                                                                                                                                                                                           A Accession: C86141
A Status: preliminary
A Molecule type: DNA
A Residues: 1-230 <STO>
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Search completed: March 7, 2002, 22:06:22 Job time: 3535 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

March 7, 2002, 22:13:04; Search time 26.04 Seconds Run on:

(without alignments) 94.337 Million cell updates/sec

Perfect score: Sednence:

US-09-665-728-1_COPY_56_122

342 1 OVIDGASRILERSLSSRSRV.....RELRQLYVQGGGDCPEMSVG Scoring table:

100059 seqs, 36664827 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

100059 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P13023 dictyosteli					P37554 bacillus su	O48556 zea mays (m		P33700 rhizobium m	Q9z9p2 bacillus ha				089046 rattus norv	P96920 mycobacteri	Q10853 mycobacteri				Q16539 h mitogen-a			Q00106 ictalurid h	P52813 anopheles g	P33271 saccharopol		9,	٣		P06856 vaccinia vi	069967 streptomyce		P09110 homo sapien
SUMMARIES	£1	RL2_DICDI	EGFR_DROME	HUPH_BRAJA	ECH8_MYCLE	IPYR_SOLTU	SP5T_BACSU	IPYR_MAIZE	ECT1_YEAST	EXOU_RHIME	GRK_BACHD	FDH_PICAN	Y545_AQUAE	CO1B_MOUSE	CO1B_RAT	EX5B_MYCTU	YK03_MYCTU	ARS1_HUMAN	ARS1_MOUSE	MK14_CANFA	MK14_HUMAN	MK14_MOUSE	GSHR_HAEIN	VG65_HSVI1	RS3A_ANOGA	CPXK_SACER	VL2_BPV1	RCSC_ECOLI	DPOL_VARV	DPOL_VACCC	DPOL_VACCV	MIAA_STRCO	CKRA_MOUSE	THIK_HUMAN
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	Query Match Length	237	1426	287	257	211	178	214	323	342	380	361	399	484	484	1094	285	348	348	360	360	360	456	1434	268	405	469	933	1005	1006	1006	312	362	424
æ	Query		•	•	7	17.5	٠	17.3	17.1	17.0	٠		•	16.7		16.5	•	ė.	٠	ė.	16.2		٠	ė.	ė.		16.1	16.1	9	ė	ė.	ď.	15.8	ď.
	Score	63.5	62.5	61.5	60.5	09 .	59.5	59	58.5	28		57.5	57	57		56.5		S	S	S	55.5	ഗ	ഗ	S	55	22	52	52	52	52		54.5	54	54
	Result No.	-	8	m	7	S	9	7	8	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	

035828 rattus norv	P57737 homo sapien	P25455 drosophila	P30236 glycine max	P35931 bluetongue	P55198 homo sapien	022537 oryza sativ	023979 hordeum vul	Q09741 schizosacch	P19623 homo sapien	Q64674 mus musculu	P27828 escherichia
W70T_RAT	W70T_HUMAN	PIP1_DROME	HS41_SOYBN	VNS1_BTV2A	AF17_HUMAN	IPYR_ORYSA	IPYR_HORVD	SPEE_SCHPO	SPEE_HUMAN	SPEE_MOUSE	WECB_ECOLI
_	-	Н	-	-	Н	-	_	-	_	_	-
443	925	1312	192	552	1093	214	215	298	302	302	376
15.8	15.8	15.8	15.6	15.6	15.6	15.5	15.5	15.5	15.5	15.5	15.5
	54	54	3.5	3,5	3.5	23	23	53	23	23	53
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ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 SRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQL-----YVQGGG--DCPEMSVG 67
                                                                                                                                                                                                                                                       Singleton C.K.; "Nucleotide sequence of V1, a ribosomal protein gene from Dictyostelium discoideum.": Nucleic Acids Res. 17:7989-7989(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18.6%; Score 63.5; DB 1; Length 237; 36.2%; Pred. No. 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ribosomal protein.
SEQUENCE 237 AA; 26298 MW; 77B736C767E35C71 CRC64;
                                                                                                                                  Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
NCBL_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGFR_DROME STANDARD; PRT; 1426 AA. P04412; 061601; Q9W2G0; P81868; 13-AUG-1987 (Rel. 05, Created) 20-BC-1989 (Rel. 37, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                            01-JAN-1990 (Rel. 13, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
60S RIBOSOMAL PROTEIN L2.
RPL2 OR RPGA OR VI.
                              237 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                              PRT;
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InterPro; IPR002171; Ribosomal_L2.
Pfam; PF00181; Ribosomal_L2; 1.
PROSITE; PS00467; RIBOSOMAL_L2; 1.
                                                                                                                                                                                                                                        MEDLINE-90016885; PubMed-2678007;
                                                             01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X15710; CAA33741.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21; Conservative
                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
STRAIN=AX3;
                              RL2_DICDI
P13023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
EGFR_DROME
               RL2_DICDI
RESULT
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DE EPIDEERAL GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (GGTR)

OR STORKER RECTORAL MERGED PROFERED, INDOSOPHILA RELATIVE OF ERBS).

OR DIOGRAPHILA MAJINGTONIA THE CONTROL OF THE CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cell 89:13-16(1997).

-I- FUNCTION: BINDS TO FOUR LIGANDS: SPITZ, GURKEN, VEIN AND ARGOS, WHICH IS AN ANTAGONIST. TRANSDUCES THE SIGANL THROUGH THE RAS-RAF-MAPK PATHWAY. INVOLVED IN A WYRIAD OF DEVELOPMENTAL DECISIONS.

CRITICAL FOR THE PROLIFERATION OF IMAGINAL TISSUES, AND FOR THE DETERMINATION OF BOTH THE ANTERO-POSTERIOR AND DORSO-VENTRAL POLARITIES OF THE COCYTE. IN THE EMBRROV, DIAKS A ROLE IN THE ESTABLISHMENT OF VENTRAL CELL FATES, MAINTENANCE OF AMNIOSEROSA AND VENTRAL NEUROECTODERMAL CELL FATES, GERM BAND RETRACTION, CELL FATE SPECIFICATION IN THE CENTRAL NERVOUS SYSTEM AND PRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTERNATIVE PRODUCTS: 3 ISOFORMS; TYPE I (SHOWN HERE), TYPE II AND TYPE III; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: UBIOUTOUSLY EXPRESSED IN EMBRYOS. IN LARVAE,
UNIFORM EXPRESSION IS SEEN IN WING DISKS, GENITAL DISK, ANLAGEN OF
TESTIS AND OVARY, AND BRAIN CORTEX. IN EYE-ANTENNA DISK, HIGHEST
EXPRESSION IS ANTERIOR TO MORPHOGENETIC FURROW, LEVELS REMAIN HIGH
IN PHOTORECEPTOR PRECURSOR CELLS. THIS PATTERN IS REVERSED IN
POSTERIOR EYE DISK. IN ADULTS EXPRESSION IS HIGH IN BRAIN CORTEX
AND THORACIC AND ABDOMINAL GANGLIA.
SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang X.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A., Yeng J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao G., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A., AND MUTATION ANALYSIS.
MEDLINE-92038942; PubMed=1936959;
Raz E., Schelter E.D., Shilo B.Z.;
"Interallelic complementation among DER/flb alleles: implications for the mechanism of signal transduction by receptor-tyrosine kinases.";
Genetics 129:191-201(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perrimon N., Perkins L.A.;
"There must be 50 ways to rule the signal: the case of the Drosophila
EGF receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN TYROSINE PHOSPHATE.
SUBCELLULAR LOCATION: ISOFORMS TYPE I AND TYPE II ARE TYPE I
MEMBRANE PROTEINS. ISOFORM TYPE III IS A TYPE III MEMBRANE
                                                                                                                                                                                                                                                                                                             STRAIN-DAEKWANRYEONG;
MEDLINE-85137938; PubMed-298332;
Wadsworth S.C., Vincent W.S. III, Bilodeau-Wentworth D.;
"A Drosophila genomic sequence with homology to human epidermal growth factor receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF052754; AAC08536.1; -.
EMBL; AF052753; AAC08536.1; JOINED.
EMBL; AF052754; AAC08535.1; -.
EMBL; AF052752; AAC08535.1; JOINED.
EMBL; K03044; AAAS1462.1; -.
EMBL; K03417; AAAS1460.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97248481; PubMed-9094709;
                                                                                                                                                                                                                                                                                         SEQUENCE OF 959-1078 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 314:178-180(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EGF receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVIEW
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FROM N.A.
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                      STRAIN-USDA 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECH8_MYCLE
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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     δy
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                                                                                                                                                                                                                                                                                                    PIR; A00640; GQFPE.

R HSSP; P11362; 1FG1.

R HSSP; P11362; 1FG1.

FlyBase: FB900003731; Egfr.

R InterPro; IPR000494; EGFR.

R InterPro; IPR000719; Euk_pkinase.

InterPro; IPR0005174; Furin-like.

R InterPro; IPR001245; Tyr_kin.

R InterPro; IPR001245; Tyr_kin.

R InterPro; IPR001245; Tyr_kin.

R Ffam; PF00069; PK10828; 1.

R Pfam; PF001030; Recep_L_domain; 2.

SMART; SM00261; FU; 7.

SMART; SM0019; TyrKci.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R ROSITE; PS00109; PROTEIN_KINASE_DOM; 1.

R TYGNSHMENTANE; Glycoprotein; Receptor; Phosphorylation; Transferase; W Tyrosine-Protein kinase; ATP-binding; Signal; Alternative splicing; W STGNII protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

BHOSPHORVLATION (BY EXC) (BY SIMILARITY).

PHOSPHORVLATION (AUTO-) (BY SIMILARITY).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPIDERMAL GROWTH FACTOR RECEPTOR EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VIDGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 62.5; DB 1; Length 1426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY). ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation update)
HYDROGENASE EXPRESSION/FORMATION PROTEIN HUPH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
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                            EMEL; AF109077; AAD261341; EMEL; AF109078; AAD261321; EMEL; AF109078; AAD261321; EMEL; AF109078; AAD261321; EMEL; AF109078; AAD261331; EMEL; AF109078; AAD261331; EMEL; AF109079; AAD261301; EMEL; AF109079; AAD261311; EMEL; AF109089; AAD261311; EMEL; AF109089; AAD261311; EMEL; AF109080; AAD261311; EMEL; AF109080; AAD261311; EMEL; AF109080; AAD261311; EMEL; AF109080; AAD261321; EMEL; AF109080; AAD26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last seq
01-FEB-1996 (Rel. 33, Last anno
                                                                                                                                                                                                                               EMBL, X02293; CAA26157.1; -
EMBL, X78920; CAA55523.1; -
EMBL, X78918; CAA55521.1; -
EMBL, X78919; CAA5552.1; -
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34.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31
869
890
938
944
971
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HUPH_BRAJA
ID HUPH_BRAJA
AC P48340;
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MOD_RES
MOD_RES
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DOMAIN
TRANSMEM
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DOMAIN
NP_BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cole S.T., Eiglmeier K., Parkhill J., James K.D., Thomson N.R., Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D., Mungall K., Basham D., Brown D., Chillingworth T., Connor R., Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N., Holroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S., Murphy L., Oliver K., Quail M.A., Rajandream M.-A., Rutherford K.M., Ruther S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R., Barrell B.G.; Woodward J.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPONENTS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: (3S)-3-HYDROXYACYL-COA = TRANS-2(OR 3)-ENOYL-COA + H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 QVIDGASRIL-----ERSLSSRSRV---IANYALVPFHDPDIGPV--TLTADPVVFQR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS TO THE ENOYL-COA HYDRATASE/ISOMERASE FAMILY.
                                      Fu C., Maier R.J.; "Organization of the hydrogenase gene cluster from Bradyrhizobium japonicum: sequences and analysis of five more hydrogenase-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - FUNCTION: COULD POSSIBLY OXIDIZES FATTY ACIDS USING SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
18.0%; Score 61.5; DB 1; Length 287;
Best Local Similarity 29.1%; Pred. No. 2.3;
Matches 23; Conservative 13; Mismatches 24; Indels 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30702 MW; 13FC69C55ED88555 CRC64;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROBABLE ENOYL-COA HYDRATASE ECHA8 (EC 4.2.1.17).
ECHA8 OR ML2402 OR MLCB1306.05C.
                                                                                                                                                                                             Gene 145:91-96(1994).
-!- SIMILARITY: BELONGS TO THE HUPH/HYAF FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Massive gene decay in the leprosy bacillus.";
Nature 409:1007-1011(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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MEDLINE=94320794; PubMed=8045431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 --- QLVSRGYGTCRVLSTG 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; L25760; AAA50823.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 AA;
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      noved. Usage by and for commercial
(See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SOLUBLE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                             2 VIDGASRI------LERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELR 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Solanum tuberosum (Potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                Query Match
17.7%; Score 60.5; DB 1; Length 257;
Best Local Similarity 27.0%; Pred. No. 2.7;
Matches 20; Conservative 7; Mismatches 28; Indels 19
                                                                                                                                      Pfam; PF00378; ECH; 1. **
PROSITE; PS00166; ENCY._COA_HYDRATASE; 1.
Fatty acid metabolism: Lyase; Complete protecome.
SEQUENCE 257 AA; 27516 MW; 258801EB690BCD00 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
: D06115FC6F2AC22A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
modified and this statement is not removed. entities requires a license agreement (See Por send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    211 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                      InterPro; IPR001753; Encyl_CoA_hydrtse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001596; Pyrophosphatase.
Pfam. PF00719; Pyrophosphatase; 1.
ProCom; PD002014; Pyrophosphatase; 1.
PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         211 AA; 24261 MW;
                                                              EMBL; Y13803; CAA74130.1; -.
                                                                              CAC31918.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; 236894; CAA85362.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                          52 QLYVQGGGDCPEMS 65
                                                                                                                                                                                                                                                                                                                                                                              | | ||:
62 ----AAGADIKEMA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Magnesium.
ACT_SITE 61 6
SEQUENCE 211 AA; 2
                                                                           AL583925; CAC:
P14604; 2DUB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASE) (PPASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                           Leproma; ML2402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-4113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPYR_SOLTU
Q43187;
                                                                              EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPYR_SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
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                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.";
J. Bacteriol. 178:4500-4507(1996).
-!-FUNCTION POSITIVE AND NEGATIVE TRANSCRIPTIONAL REGULATOR OF SIGNER OF PERDENDENT GENES. MAY PROVIDE A MECHANISM OF FEEDBACK CONTROL THAT IS IMPORTANT FOR FORESPORE DEVELOPMENT.
-!- SIMILARITY: STRONG, TO B.SUBTILIS ABRB AND ABH. SOME, TO M.TUBERCULOSIS RV2595.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bagyan I., Hobot J., Cutting S.M.;
"A compartmentalized regulator of developmental gene expression in
                                                                                                                                                                                                                                                                                                                                                                                                               Ogasawara N., Nakai S., Yoshikawa H.; "Systematic sequencing of the 180 kilobase region of the Bacillus subtilis chromosome containing the replication origin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99 SEMLERTMDQRSSVLESDAKSVQLVNGIDEDMNSYTVGPIVANGDPIGAVVIFSKD 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 SRILERSLSSRSRVIANYA----LVPFHDPD-----IGPVTLTADP----VVFQRE 49
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SubtiList; BG10119; spovT.
Transcription regulation; DNA-binding; Repressor; Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 178;
 Length 211;
                                12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Complete proteome.
178 AA; 19742 MW; 19418022DD371180 CRC64;
                                                             6 ASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVF 46
                                                                               14 APRLNERILSSISR--RSVAAHPWHDLEIGPEA----PSVF 48
                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
 DB 1;
2.5;
                                                                                                                                                                                                    (Rel. 30, Created)
(Rel. 30, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ¥.
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32.1%; Pred. No. 2.4;
ive 10; Mismatches
                                4; Mismatches
                                                                                                                                                                         178
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Score 60;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-96051385; PubMed-7584024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-96345614; PubMed-8755877;
                                                                                                                                                                                                                                                     STAGE V SPORULATION PROTEIN T
 17.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; D26185; BAA05291.1; -. EMBL; Z99104; CAB11832.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19; Conservative
                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Res. 1:1-14(1994).
 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                FROM N.A.
                                                                                                                                                                                                                                                                                     Bacillus subtilis,
                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sporulation;
SEQUENCE 1
                                                                                                                                                                                                     01-OCT-1994
01-OCT-1994
                                                                                                                                                                                                                                      20-AUG-2001
                                                                                                                                                                        SP5T_BACSU
P37554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPYR_MAIZE
048556;
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                Best Loca
Matches
                                                                                                                                                           SP5T_BACSU
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STRAIN-1021
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Best Local S
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                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
SOLUBLE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
                                                                                      Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93233657; Pubmed-8474454;
HOTOWITZ D.S., Abelson J.N.;
The US small nuclear ribonucleoprotein particle protein involved only
in the second step of pre-mRNA splicing in Saccharomyces
                                                                                                                                                                            STRAIN-CV. B73;
Kadambi S.N., Baysdorfer C.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)0 = 2 ORTHOPHOSPHATE.
-!- COPACTOR: MAGNESIUM DEPENDENT (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTIDYLYLTRANSFERASE).
MUQ1 OR ECT1 OR YGR007W OR G3856.
Saccharomyces cerevisione (Baker's yeast).
Saccharomyces cerevisione, Saccharomycetes;
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
9
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20-A0G-2001 (Rel. 40, Last annocation update)
ETHANOLARINE-PHOSPHATE CYIDYLIVITRANSFERASE (EC 2.7.7.14)
(PHOSPHORYLETHANOLAMINE TRANSFERASE) (CTP:PHOSPHOETHANOLAMINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 59; DB 1; Length 214; Pred. No. 3.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            r SIMILARITY.
F70E726561257AB9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 ASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVF 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           323 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF034947; AAB88618.1; -.
InterPro; IPR001596; Pyrophosphatase.
Pfam; PF00719; Pyrophosphatase; 1.
ProDom; PD002014; Pyrophosphatase; 1.
PROSITE; PS00387; PPASE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mol. Cell. Biol. 13:2959-2970(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECTI_YEAST STANDARD; P33412; Q05725; 01-FEB-1994 (Rel. 28, Created) 01-FEB-1994 (Rel. 28, Last seq)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 AA; 24370 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Magnesium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                      [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
ECT1_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GASRILERSLSSRS-----RVIANYALVPFHDPDIGPVT-----LTADPV-----VFQ 47
                                                                                                                                                                                                                                                                                                                                                                                                         -i- PATHWAY: PHOSPHOLIPID BIOSYNTHESIS; CDP-ETHANOLAMINE SYNTHESIS; SECOND STEP.
-i- SIMILARITY: BELONGS TO THE CYTIDYLYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                      J. Biochem. 120:1040-1047(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid pSymB (megaplasmid 2).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; B480b/; proc. SGD: $3003239, MuQ1.
InterRco: IPR01994; Cytidylyltransf.
InterRco: Yctidylyltransf; 1.
Fransferase; Nucleotidyltransferase; Phospholipid biosynthesis.
DOMAIN 1 165 CATALYIC (POTENTIAL).
ACANTICT 252 S -> I (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 323;
                                                                                                                                                                                       Min-Seok R., Kawamata Y., Nakamura H., Ohta A., Takagi M.;
"Isolation and characterization of ECT1 gene encoding CTP:
phosphoethanolamine cytidylyltransferase of Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
Hebling U., Hofmann B., Delius H.; Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FED-1994 (Rel. 39, Last annotation update)
SUCCINGGLYCAN BIOSYNTHESIS PROTEIN EXOU (EC 2.-.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.1%; Score 58.5; Di
27.8%; Pred. No. 6.3;
iive 12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342 AA
                                                                                                SEQUENCE FROM N.A., AND CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
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                                                                                                                                                                MEDLINE=97137537; PubMed=8982874;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; L03536; AAA34916.1; -. EMBL; Z72792; CAA96990.1; -. EMBL; D50644; BAA09310.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RDLDNVLVNGGYKFDAEDC 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         CDP-ETHANOLAMINE.
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                                                                                                                                     STRAIN-GRF88
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DEHYDROGENASE) (FDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-4905;
                                                                                           GLYCERATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 EMSVG 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 EAEYG 79
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                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                    *Monalysis of the Rhizobium meliloti genes exoU, exoV, exoW, exoT, and exoI involved in exopolysaccharide biosynthesis and nodule invasion: exoI involved in exopolysaccharide biosynthesis and nodule invasion: exoU and exoW probably encode glucosyltransferases.";
Mol. Plant Microbe Interact. 6;735-744(1993).

-I FUNCTION: GLYCOSYLTRANSFERASE REQUIRED FOR THE SYNTHESIS OF SUCCINOGLYCAN (EPS I). NEEDED FOR THE ADDITION OF THE SIXTH SUGAR (GLUCOSE). CATALYZES THE FORMATION OF A BETA-1,6 LINKAGE BETWEEN THE FIFTH AND SIXTH SUGAR.

-I PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS.

-I SUBCELLULAR LOCATION: CYTOPLASMIC.

-I SUBCELLULAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 DGASRI-LERSLSSRSRVIA-NYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGD 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sasaki R., Masui N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-C-125 / JCM 9153;
MEDLINE-99184645; PubMed-10086841;
Takami H., Nakasone K., Hirama C., Takaki Y., Masui N., Fuji F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; D49348; D49348.
InterPro; IPR001173; Glycos_transf_2.
Pfam; PF00535; Glycos_transf_2; 1.
Transferase; Glycosyltransferase; Exopolysaccharide synthesis;
                            STRAIN-RCR2011 / SU47;
MEDLINE-94162682; Pubmed-8118055;
Becker A., Kleickmann A., Kuester H., Keller M., Arnold W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., M.
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     342 AA; 37017 MW; EAF55E0EBDA023BC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRK_BACHD STANDARD; PRT; 380 AA. 0929F2; 09KFC9; 1 (Rel. 40, Created) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) GLXK OR BH0555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.0%; Score 58; Interity 37.3%; Pred. No. 7. Conservative 5; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-C-125 / JCM 9153;
MEDLINE-20512582; Pubmed-11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L20758; AAA16053.1; -. EMBL; Z22646; CAA80359.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-189 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-C-125 / JCM 9153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus halodurans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
les 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-86665;
                                                                               Puehler A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Horikoshi K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
GRK_BACHD
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hollenberg C.P., Janowicz 2.;

**Mona-molecules coding for FMDH control regions and structured gene for a protein having FMDH-activity and their uses.";

**Patent number EP0299108, 18-JAN-1989.**

-! CATALYTIC ACTIVITY: FORWATE + NAD(+) = CO(2) + NADH.

-! SUBUNIT: HOMODIMER.

-! SUBUNIT: BELONGS TO THE D-ISOMER SPECIFIC 2-HYDROXYACID DEHYDROGENASES FAMILY. STRONG, TO OTHER FDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakamura Y., Inoue A.;
"An improved physical and genetic map of the genome of alkaliphilic
Bacillus sp. C-125.";
                                                                Extremophiles 3:21-28(1999).
-!- CATALYTIC ACTIVITY: ATP + (R)-GLYCERATE - ADP + 3-PHOSPHO-(R)-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 ASRILERSLSSRSRVI--ANYALVPFHDPDIGPVTLTADPVVFORELRQLYVQGG-GDCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pichia angusta (Yeast) (Hansenula polymorpha).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Pichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 58; DB 1; Length 380;
Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
FORMATE DEHYDROGENASE (EC 1.2.1.2) (NAD-DEPENDENT FORMATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Transferase; Kinase; Complete proteome.
SEOUENCE 380 AA; 39955 MW; 0C6E227253B3E46D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002162; D_2_hydroxyacid_DH.
                                                                                                                                                                                                                                                                                                                                                       EMBL; AP001508; BAB04274.1; -. EMBL; AB013375; BAA75390.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.0%;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003747; DUF168.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00389; 2-Hacid_DH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; A06214; CAA00531.1; -. HSSP; P33160; 2NAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 35.4 Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRR BERTHANDER
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98196666; PubMed-9537320;
Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
Deckert G., Warren P.V., Snead M.R., Keller M., Aujay M., Huber Peldman D.E., Overbeek R., Snead M.R., Keller M., Aujay M., Huber Peldman R.A., Short J.M., Olson G.J., Swanson R.V.;
"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
                                                                                                                                                                         6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10;
                                            PROBABLE.

Mad (ADP PART) (BY SIMILARITY).

SUBSTRATE-BINDING (BY SIMILARITY).

OFC001366F9E479B CRC64;
                                                                                                                                                            4 DGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGG
                                                                                                              Length 361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 57; DB 1; Length 399;
Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        al.protein; Complete proteome.
399 AA; 46953 MW; AA57D8680674318B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150 DG-EKVMEKALVDVRKVLADYE------GPVVITEDKVIY 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 DGASRILERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVF 46
                                                                                                               DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COIB_MOUSE STANDARD; PRT; 484 AA. 09WUM3; 09CVA2; 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                               Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBI_TaxID=63363;
                                                                                                              16.8%; Score 57.5; DE ilarity 26.8%; Pred. No. 9.5; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11; Mismatches
PROSITE; PS00065; D_2_HYDROXYACID_DH_1; PROSITE; PS00670; D_2_HYDROXYACID_DH_2; PROSITE; PS00671; D_2_HYDROXYACID_DH_3;
                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last seque 20-AUG-2001 (Rel. 40, Last seque 20-AUG-2001 (Rel. 40, Last annoment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE000695; AAC06792.1; -.
                                                                              361 AA; 39779 MW;
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                                                                                                                                                                                                                                                                                                  HYPOTHETICAL PROTEIN AQ 545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 30.2%
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 392:353-358(1998).
                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORONIN 1B (CORONIN 2).
                                           199
                                Oxidoreductase; NAD.
INIT_MET 0 0 0
NP_BIND 164 199
ACT_SITE 257 257
SEQUENCE 361 AA; 39
                                                                                                              Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                         Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 35
                                                                                                                                                                                                                                          Y545_AQUAE
O66822;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 13
CO1B_MOUSE
                                                                                                                                                                                                                               Y545_AQUAE
                                                                                                                                                                                                                    RESULT
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 SORPE
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CE NAME ALLEGATE (MOLUSE).

CENARATORIS RECEASE, CHORAGELS, CENISTA, VETEBERAL ENLERGESCONI;

CENARALIA, ENTHERIAS ROCHILIS, SCINTOGNACHI, MALIDAGE, MATINAS;

KNELLARD-10090;

KNELLARD-101000;

KNELLARD-101000;

RESPONDANCE READ AND C., MONG S., Redders M. Thomas M.L.;

RECOLUMNIA M. KNIL C., MONG SENERAL M. Thomas M.L.;

RECOLUMNIA M. KNIL C., MONG SENERAL M. Thomas M.L.;

NAME AND C., MONG SENERAL M. AND C. MONG S., Redders C. AND C. MONG S., Redders C. Local Bold, T. TASPING SENERAL M. AND C. MONG S., Redders M. THAR A. MONG S., TASHIRAR M. YORKHILAND M. THAR A. MARWAL M. MARWAL MARWAL MARWAL MARWAL MA
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Score 57; DB 1; Length 484; Pred. No. 15;

16.7%;

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25 ALVPFHDPDIGP--VTLTADPVVFQRELRQLYVQ---GGGD----CPEMSV
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Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bishai W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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3
                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
        Gaps
                                                                                                                                                                                                                                                                                                                                                           5 GASRILERSL-----SSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
      16;
                                                   Score 57; DB 1; Length 484;
Pred. No. 15;
                             10 LERSLSSRSRVIANYALVPFHDPDIGPVTLTADPVVFQRELRQLYVQGGGD
      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 15;
6; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COILED COIL (POTENTIAL). 746EDF119680EBBF CRC64;
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InterPro; IPR001680; WD40.
Pfam; PF00400; WD40; 3.
SWART: SM0030; WD40; 3.
PROSITE; PS00678; WD_REPEATS_1; 1.
PROSITE; PS50082; WD_REPEATS_2; 2.
PROSITE; PS50084; WD_REPEATS_2; 2.
PROSITE; PS50094; WD_REPEATS_2; 2.
PROSITE; PS50094; WD_REPEATS_2; 2.
PROSITE; PS50094; WD_REPEATS_2; 2.
PROFILE; PS50094; WD_REPEATS_2; WD_REPEATS_2; WD_REPEATS_2; WD_REPEATS_2; WD_REPEATS_2
                                                                                                                                                                              20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CORONIN 1B (CORONIN 2).
   Mismatches
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WD 2.
WD 3.
WD 4.
   9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.78; 29.48;
 Conservative
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                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20; Conservative
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265
447
484 AA;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 LYVQGGGD 60
16;
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                                                                                                                                                 CO1B RAT
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SEQUENCE
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Matches
                                                                                                                 RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
EX5B_MYCTU
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                                                                                                                                CO1B_RAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Elsen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weldman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ۵.
                                                                                                                                                                                                                                                                                                                                                                            STRAIN=H37RV;

MEDLINE=98295987; PubMed=9634230;

MEDLINE=98295987; PubMed=9634230;

A Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,

Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,

Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

A Hornsby T., Jagels K., Skelton S., Squares S., Squares R.,

Rutter S., Seeger K., Skelton S., Squares R.,

Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;

"Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tuberculist, Rv0630c; -.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
                                                                                                                                                                         Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: REQUIRED FOR EFFICIENT DNA REPAIR; IT CATALYZES THE UNWINDING OF DOUBLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND THE CLEAVAGE OF SINGLE-STRANDED DNA AND IT STIMULATES LOCAL GENETIC RECOMBINATION.
ALL OF THESE ACTIVITIES REQUIRE CONCOMITANT HYDROLYSIS OF ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATP (POTENTIAL).
FW; 31262D376875C201 CRC64;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EXONDEX/RIBONUCLEASE V BETA CHAIN (EC 3.1.11.5)
RECB OR RV0630C OR MT0658 OR MTCY20H10.11C.
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33.3%; Pred. No. 45;
tive 9; Mismatches
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HSSP; P56255; 2PJR.
TIGR; MT0658; -.
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SEQUENCE 1094 AA;
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Indels

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Search completed: March 7, 2002, 22:13:06 Job time: 459 sec

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13

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Run on:

March 7, 2002, 22:07:47 ; Search time 65.89 Seconds
 (without alignments)
 148.736 Million cell updates/sec

US-09-665-728-1_COPY_56_122 342 1 QVIDGASRILERSLSSRSRV.....RELRQLYVQGGGDCPEMSVG 67 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

473505 segs, 146272329 residues Searched:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

473505

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SPTREMBL_17:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:* sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:* sp_plant:* sp_rodent:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ID	076518	092108	09JHA8	09UMP9	09Y334	09M109	080725	09XCV7	012395	09UBD9	090ZM3	006693	09ABL3	Q9FDU0	049749	09SY12	201060	OGHEGO	00000	611667
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Score	175	131.5	131.5	131	131	71.5	70.5	65.5	65	63	63	63	62.5	62.5	62	62	61.5	61	19	1
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2 053937 4 099773	12 Q9QQM9 5 Q9VR40	10 082597	10 Q9MAM9	11 Q9D1L8	3 093982	5 Q9NA54	4 Q9HAL4	1 Q9H0K9	5 096252	01MS60 01	2 Q9KY85	028762	10 040771	3 Q9UQY5	10 Q9FUA4		P73158	l Q9H401	090060	1 Q9P3Q9	2 O9RMP5	Q9NSK3	.2 Q9YMT9
285	669	216	230	290	380	385	443 4	702 4	130	215	365	552	275	354	373]	•	237	511 4	1820	114 3	192	283 4	359 1
17.7	17.7	17.5	17.5	17.5	17.4	17.4	17.4	17.4	17.3	17.3	17.3	17.3	17.1	17.1	17.1	17.1	17.0	17.0	16.8	16.7	16.7	16.7	16.7
60.5	60.5	9	9	9	59.5	59.5	59.5	59.5	29	29	59	29	58.5	58.5	58.5	58.5	28	28	57.5	57	57	57	57
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SEQUENCE FROM N.A.
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STRAIN=C57BL/R1J, AND BALB/C; TISSUE=BRAIN;
MEDLINE-98211706; PubMed-9551980;
Snoek M., Teuscher C., van Vugt H.;
Molecular analysis of the major MHC recombinational hot spot located
within the G7c gene of the murine class III region that is involved in
disease susceptibility.";
Ji Immunol. 160:266-272(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-C57BL/RIJ, AND BALB/C; TISSUE-BRAIN;
MEDLINE-20260998; PubMed-10803853;
Snoek M., Albertella M.R., van Koolj M., Wixon J., van Vugt H.,
de Groot K., Campbell R.D.;
"G7c, a novel gene in the mouse and human major histocompatibility
complex class III region, possibly controlling lung tumor
                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Euteleostom1;
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"Characterisation of the novel gene G7c located in the class III region of the human Major Histocompatibility Complex.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.5%; Score 131.5; DB 11; Length 891; 47.5%; Pred. No. 1.7e-07; tive 9; Mismatches 21; Indels 1;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95983 MW; 1EA26B5121118720 CRC64;
                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                891 AA.
                                                                                                                                          Created)
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susceptibility.";
Immunogenetics 51:83-386(2000).
EMBL; AF134318; AAF69177.1;
EMBL; AF134319; AAF61401.1;
InterPro; IPRQ02035; vWFA.
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                                                                                                                                     01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 47.5
les 28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002035;
SMART; SM00327; VWA;
SEQUENCE 891 AA;
                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
                                                                                                                                                                                                                        G7C (G7C PROTEIN).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 51.2%; Score 175; DB 5; Length 5198; Best Local Similarity 45.5%; Pred. No. 6.6e-12; Matches 30; Conservative 16; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 5198 HEMICENTIN.
1462 5198 MISSING (IN ISOFORM F15G9.4A).
5198 AA; 570816 MW; DA8511FF2B58D37B CRC64;
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Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AR109905; AAC84152.1;
InterPro; IRR002035; VWFA.
SMART; SM00327; VWA; 1.
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SEQUENCE 873 AA; 94894 MW; 5761E3620F8D831C CRC64;
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01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 94.9 KDA PROTEIN.
Mus musculus (Mouse).
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BPD_transp.
EGF-like.
                                                 Interpro; IPR001881; EGF_Ca.
Interpro; IPR003598; Ig_C2.
Interpro; IPR003600; Ig_Ilke.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003005; vWFA.
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5198
5198
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SEQUENCE FROM N.A.
MEDLINE=96411681; PubMed=8812450;
Albertella M.A., Jones H., Thomson W., Olavesen M.G., Campbell R.D.;
"Localization of eight additional genes in the human major
histocompatibility complex, including the gene encoding the casein
kinase II beta subunit (CSNK2B).";
Genomics 36:240-251(1996).
                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Б.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 ASRILERSLSSRSR----VIANYALVPFHDPDIGPVTLTADPVVFORELRQLYVQGGGDC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rowen L., Qin S., Madan A., Dickhoff R., Dors M., Madan A., Hicks
Loretz C., Ratcliffe A., Abbasi N., Shaffer T., Hood L.,
"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                               Albertella M.R.;
Thesis (1997). University of Oxford, Department of Biochemistry,
MRC: Immunochemistry Unit.
EMBL: AJ245418; CAB52192.1; -.
                                                                                                                                                                                                                                                                                                                                                               Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.3%; Score 131; DB 4; Length 852; 44.4%; Pred. No. 1.9e-07; ive 10; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                    21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF134726; AAD21820.1; --
SEQUENCE 852 AA; 92538 MW; 025430B3F912A941 CRC64;
                                                                                                                                                                                                                                                                                                  57837 MW; B32D8DD8E24BD06D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                           38.3%; Score 131; DB 4; 44.4%; Pred. No. 1.1e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                  10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sapiens (Human).
                                                                                                                                                                                                                                                                           536 5
536 AA;
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                             SEQUENCE FROM N.A.
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|PEM 394
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SEQUENCE
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Q9Y334;
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Q9M1Q9;
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Matches
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Arabidopsis.
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SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Rounsley S.D., Lin X., Fraser C.M., Somerville C.R., Venter J.C.,
"Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC
TRANSPORTERS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC
TRANSPORTERS).
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

Rieger M., Mueller Auer S., Zipp M., Schaefer M., Mewes F.

Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
      Last annotation update)
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29.1%; Pred. No. 6;
live 10; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9 ILERSLSSRSRVIANYALVPFHDPDIGPVTL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AL138651; CAB71875.1;
InterPro; IPR003593; AAA.
InterPro; IPR001140; ABC_transporter_tmem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00211; ABC_TRANSPORTER; 2.
PROSITE; PS00095; C5_MTASE_2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR001525; C5_DNA_meth.
Pfam; PF000664; ABC_membrane; 2.
Pfam; PF000055; ABC_tran; 2.
SMART; SM00382; AAA; 2.
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01-JUN-2001 (TrEMBLrel. 17, P-GLYCOPROTEIN-LIKE PROETIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49 ELRQLYVQG-GGDCPEMSV 66
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HSSP; P13569; 1NBD.
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F14M4.17.
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Best Local Similarity
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Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delius H., Hebling U.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                           (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                 YLR128W OR L3111 OR L9233.2.
                                                                    PRELIMINARY;
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STRAIN-S288C (AB972);
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01-NOV-1996 (
01-JUN-2001 (
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                                                                  Q12395
Q12395;
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                                                                                                                                                                                                                                                                                                                                                                               9 ILERSLSSRSRVIANYALVPFHDPDIGPVTL------TADPVVFQR 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kulowski K., Wendt-Pienkowski E., Han L., Yang K., Vining L.C.,
Hutchinson C.R.;
                                                                                                                                                                                                                                                                                        Length 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19.2%; Score 65.5; DB 2; Length 584; 27.8%; Pred. No. 13;
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                                                                                                                                                                                                                           139027 MW; 97D2A8AFEBA698E6 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                          DB 10;
InterPro: IPR001140; ABC_transporter_tmem.
InterPro: IPR0018439; ABC_transportr.
InterPro: IPR001803; ABC_transportr.
InterPro: IPR001803; APC_ETP_A.
InterPro: IPR001852; CS_DNA_meth.
Pfam; PF00064; ABC_membrane; 2.
Pfam; PF00065; ABC_tran; 2.
PR031TE; PS00211; AAA; 2.
PR031TE; PS00211; AAA; 2.
PR051TE; PS00211; ABC_TRANSPORTER; 2.
PR051TE; PS0095; CS_MTASE_2; UNKNOWN_1.
SEQUENCE 1286 AA; 139027 MW; 97D2ABAFEBA6
                                                                                                                                                                                                                                                                                          20.6%; Score 70.5; DE
27.8%; Pred. No. 7.9;
iive 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          584 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Am. Chem. Soc. 0:0-0(1999).
-!- COFACTOR: BIOTIN (BY SIMILARITY).
EMBL; AF126429; AAD37851.1; -.
HSSP: P24182: 1BNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Created)
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InterPro; IPR000089; Biotin_lipoyl.
InterPro; IPR000901; CPSase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00364; biotin_lipoyl; 1. Pfam; PF00289; CPSase_L_chain; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1133 TIRANIAYGKGGDASESEI 1151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         440 IETEFVNEIKPFAPAGEAD 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 -- VVFQRELRQLYVQGGGD 60
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Best Local Similarity 27.89
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Streptomyces venezuelae.
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                                                                                                                                                                                                                                                                                                                 Best_Local Similarity
Matches 22; Conserv
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STRAIN—S28BC (AB972);
STRAIN—S28BC (AB972);
Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
Johnston M., Andrews S., Brinkman R., Cooper J., Kirsten J., Kucaba T.,
Hallsworth K., Hawkins J., Hiller L., Jier M., Johnson D.,
Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
Miller N., Nahn M., Pauley A., Peluso D., Rifken L., Riles L.,
Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
Wilson R., Waterston R.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.0%; Score 65; DB 3; Length 269; 32.7%; Pred. No. 5.8; cive 10; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 LERSLSSRSRVIANYALVPFHDPDIG----PVTLTADPVVFQRELRQLY 54
                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CBD829C941466180 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL, X89514; CAA61706.1; -. EMBL, X91258; CAA62639.1; -. EMBL, Z73300; CAA97697.1; -. EMBL, U53877; AAB82374.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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SEQUENCE 269 AA; 323
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C (AB972);
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Best Local Similarity
Matches 16; Conserv
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ID Q5
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MEDLINE-21173698; PubMed=11259647;

Mierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E., Eisen J., Heldelberg J.F., Alley M.R.K., Ohta N., Maddock J.R., Potocka I., Nelson W.C., Powton A., Stephens C., Phadke N.D., Ely B., DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H., Kolonsy J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K., Utterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O., Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.; "Complete genome sequence of Caulobacter crescentus."; Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).
                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=ATCC 33653;
MEDLINE=97274002; PubMed=9128176;
Kim G.T., Lee J.Y., Huh S.H., Yu J.H., Kong I.S.;
"Nucleotide sequence of the vmhA gene encoding hemolysin from Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=674;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Caulobacter group; Caulobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18.4%; Score 63; DB 2; Length 744; 39.7%; Pred. No. 34; 1ve 6; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochim. Biophys. Acta 1360:102-104(1997).
EMBL: 068271; AABS8389.1; -.
InterPro; IPRO00772; Ricin_B_lectin.
InterPro; IPRO01340; Hemlysn_pore.
PFGam; PF00652; Ricin_B_lectin; 1.
SMART; SMO458; RICIN; 1.
SEQUENCE 744 AA; 83087 MW; E7E71F4FC8B83F89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29415A726A3BF753 CRC64;
                                                                                                                                                                                   Last sequence update)
Last annotation update)
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                     82
                                                                                                                         744 AA.
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Created)
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Receptor; Complete proteome.
SEQUENCE 687 AA; 72786 MW;
                                                                                                                                                           01-JUL-1997 (TrEMBLrel. 04, 01-JUL-1997 (TrEMBLrel. 04, 01-JUN-2001 (TrEMBLrel. 17, HEAT-LABILE HEMOLYSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.7%
Matches 23; Conservative
                                                                                                                       PRELIMINARY;
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                                                                                                                                                                                                                                                             Vibrio mimicus.
                                                                                                                                                                              01-JUL-1997
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006693
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Q9ABL3
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                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=99432254; PubMed=10500198;
Senaldi G., Varnum B.C., Sarmiento U., Starnes C., Lile J., Scully S.,
Guo J., Elliott G., McNinch J., Shaklee C.L., Freeman D., Manu F.,
Simonet W.S., Boone T., Chang M.S.,
"Novel neurotrophin-1/8 cell-stimulating factor-3: A cytokine of the
IL-6 family.",
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDILINE-99382254; Pubmed-10448081;
Shi Y., Wang W., Yourey P.A., Gohari S., Zukauskas D., Zhang J.,
Ruben S., Alderson R.F.;
"Computational EST database analysis identifies a novel member of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scully S.,
inu F.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse).
Sukaryota, Metazoa, Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Pred. No. 8.2;
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                         01-WAY-2000 (TremBirel. 13, Last sequence update) 01-WAY-2000 (TremBirel. 13, Last annotation update) NEUROTROPHIN-1/B-CELL STIMULATING FACTOR-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
NEUROTROPHIN-1/B-CELL STIMULATING FROTOR-3.
                                                                                                                                                                                                                                                                                                                                    Proc. Natl. Acad. Sci. U.S.A. 96:11458-11463(1999).
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EMBL: AR176913: AAF00993.1; -.
MGD; MGI:1930088; Bsf3.
SEQUENCE 225 AA; 25261 MW: 68R1FFBABB7F1A0EA ATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neuropoietic cytokine family,";
Biochem. Biophys. Res. Commun. 262:132-138(1999).
EMBL; AF176912; AAF00992.1;
EMBL; AF172854; AAD54284.1;
EMBL; AF1778911; AAF00991.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AA.
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5; Mismatches
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          01-MAY-2000 (TrEMBLrel. 13, Created)
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Best Local Similarity 38.9%;
Matches 14; Conservative
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Best Local Similarity 38.9%;
Matches 14; Conservative
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                                                                                         Homo sapiens (Human).
                                                                                                                                                 NCBI_TaxID=9606;
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SEQUENCE

0902M3 RESULT 11 Q9Q2M3

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IL-6 family.

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SEQUENCE
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involved in the biosynthesis of the cyclic heptapeptide microcystin.";
J. Biochem. 127:779-789(2000).
                                                     Gaps
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                                                                                                                                                                                                                                                                                                                         STRAIN*K-139;
MEDLINE-20250836; PubMed-10788786;
Nishizawa T., Ueda A., Asayama M., Fujii K., Harada Ki., Ochi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nishizawa T., Asayama M., Fujii K., Harada K., Shirai M.;
"Genetic analysis of the peptide synthetase genes for a cyclic heptapeptide malcrocystin in Microcystis spp.";
J. Blochem. 126:520-529(1999).
EMBL, AB035549; BAB12211.1;
InterPro; IPR0001227; Acyltransf_domain.
InterPro; IPR000953; AMP-bind.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6
              13;
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              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E55AA358264FEC2F CRC64;
                                                                                                                                                                                                                                                                       Bacteria; Cyanobacteria; Chroococcales; Microcystis
                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
U-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
POLYKEITDE SYNTHASE AND PEPTIDE SYNTHETASE.
              24;
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                                                                                                                                                                          PRT; 3487 AA
  Pred. No. 36;
8; Mismatches
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InterPro; IPR001601; Weth-transf.
InterPro; IPR003880; Phosphopant_attach.
InterPro; IPR000051; SAM_bind.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00698; Acyl_transf; 1. Pfam; PF00202; aminotran_3; 2.
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32.8%;
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  Best Local Similarity 32.8
Matches 22; Conservative
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                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                              Microcystis aeruginosa
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Best Local Similarity
Matches 19; Conserv
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SEQUENCE 3487 AA:
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                   111 ::1
232 RQLALEG 238
                                                                                                                                                                                                                                                                                    NCBI_TaxID=1126;
                                                                                    51 RQLYVQG 57
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049749
ID 049749
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiphantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyladons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Sidler M., Dudler R.;
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY (ABC TRANSPORTERS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24;
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83;
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01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, Y19990; CAA75922.1; -.
InterPro; IPR003593; AAA.
InterPro; IPR00110, ABC_transporter_tmem.
InterPro; IPR0011043; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
InterPro; IPR00155; C5_DNA_meth.
Pfam; PF00664; ABC_membrane; 2.
Pfam; PF00605; ABC_tran; 2.
SMART; SM00382; AAA; 2.
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                                                                                    P-GLYCOPROTEIN-LIKE PROTEIN
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Best Local Similarity 26.2%
Matches 21; Conservative
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Search completed: March 7, 2002, 22:07:49 Job time: 3167 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Rat cDNA clone P00	Nephila clavipes s	Nephila clavipes s	N. clavipes spider	N.clavipes draglin	Human transporter	Human tumour suppr	Codon-optimised RA	Triticum sp. cyste	Maize caffeoyl-CoA	Human TLE-2 dene.
		ID	AAF82464	AAT85356	AAV23249	AAZ38195	AAQ14183	AAD09568	AAH23688	AAV41730	AAV82459	AAX25208	AAQ62176
		98	22	18	19	21	12	22	22	19	20	20	15
		Match Length DB	1031	2004	2338	2338	2338	2745	9063	1260	1747	1160	2271
æ	Query	Match	100.0	5.0	4.9	4.9	4.6	4.2	4.1	4.0	4.0	4.0	3.9
		Score	1031	51.6	50.4	50.4	47.2	43.4	41.8	41.2	41	40.8	40.4
	Result	No.	-	7	٣	4	2	9	7	80	o 0	10	11

(SCIO-) SCIOS INC.

5334 Human TLE-2	2682 New DNA sequence	New DNA sequence		3078 D86074 cDNA clone	J752 DNA-polymerase con			5573 Bovine alpha1(I)	7472 Sorghum bicolor	0337 Wheat raffinose			Human gas6-		3250 Nephila clavipes		Ś		9349 Sorangium cellulos				S.1		0757 Micromonospora		-		Human GCR9 co	5 Human	6 Human tyrosin	
5 AAO4533			·	·	5 AAQ80752	3 AAV65782) AAV63403		3 AAV5747	L AAD0033	2 AAS08699	1 AAQ40461		2 AAQ14184	3 AAV23250	1 AAZ38196		L AAA29550	L AAA29349	•	-	-	3 AAT70153	-	2 AAF30757			1 AAA30778	_	-	1 AAC6607	ירששאיני ט
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ALIGNMENTS

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Rat; secreted factor; P00210D09; cardiant; nephrotropic; antlinflammatory; gene therapy; cardiac disease; renal disease; inflammatory disease; ss.
                                                                                                                                       /*tag= a
/product= "Rat secreted factor"
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/*tag= b
159..923
                                                                                                                         Location/Qualifiers 96..923
              BP.
              AAF82464 standard; cDNA; 1031
                                                                                                                                                                                                                           27-SEP-2000; 2000WO-US26582.
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                                             (first entry)
                                                           Rat cDNA clone P00210D09.
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                                                                                                          Rattus norvegicus.
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                                            29-JUN-2001
                                                                                                                                                       sig_peptide
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                             AAF82464;
      AAF82464
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RESULT
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                                                                                                                                                       The present sequence encodes a novel secreted factor. The invention relates to a polypeptide comprising a sequence of at least 80% identity to residues 22-132 of a 275 anino acid sequence, or a sequence encoded by a nucleic acid hybridising under stringent conditions to the complement of the coding region comprising 1031 nucleotides, and having at least one biological activity of the polypeptide encoded by clone p00210009. The polypeptides and polynucleotides of the invention are useful for the treatment of cardiac, renal and inflammatory diseases. The polynucleotides are useful in antisense mediated gene inhibition and in gene therapy. The polypeptides are useful in assays for identifying lead compounds that may be used as therapeutic agents in the treatment of cardiac, kidney or inflammatory diseases.
                                                                               Novel secreted factor encoded by clone P00210D09 useful for diagnosing, treating and/or preventing various cardiac, renal and inflammatory
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                                                                                                                                  Claim 1; Fig 2; 69pp; English.
               Kapoun
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Best Local Similarity
Matches 1031; Conserv
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                                                                                                                                                                                                                                                                                      absorber; body armour; heavy metal; biological weapon; chemical; flavour; fragrance; Nephila clavipes; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New opt. multimerised DNA sequences encoding spider silk protein contg. both repetitive and non-repetitive sequences, useful for making high strength films, fibres, woven articles etc.
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910S-0684819 95US-0425069

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/product= "spider silk protein 1"
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The present sequence encodes a spider silk protein from the present invention. Spider silk proteins, and peptide fragments within the proteins, can be produced and purified independently and can then be mixed and made into fibres that have higher tensile strengths and elasticity than naturally occurring fibres. The fibres can be used in mixed composites. The invention allows the two naturally occurring Nephila clavipes silk proteins to be produced independently so that they can later be combined to form silk fibres of high tensile strength
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gctacctggcttttgaggagatcgcctccaccagttctggccaagtgttccagctggaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agcagcaggtgtcgaaggtgttaaagtgggtggagtccgccatccaggcctccaaagttc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2338;
                                                                                                                                                                                               Recombinant spider silk proteins - useful for making fibres
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2338 BP; 564 A; 432 C; 918 G; 424 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4.9%; Score 50.4; DB 19;
49.3%; Pred. No. 0.01;
tive 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N. clavipes spider silk protein 1 encoding cDNA.
                                                                                                                                                                                                                                                         Example 3; Column 25-30; 68pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    699 acaaggtgctggacaaggagctggagca 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 49.3
Matches 132; Conservative
                                                          Lewis RV,
(UYWY-) UNIV WYOMING
                                                                                                              WPI; 1998-270437/24.
                                                                                                                                                P-PSDB; AAW53346
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                                                          Hinman MB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             08-MAR-2000
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/product- silk protein

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10-SEP-2001
                                                                                     18-APR-1991;
                                                                                                                   20-APR-1990;
                                                         23-OCT-1991
                             EP452925-A
                                                                                                                                                                              Lewis RV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD09568
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                                                                                                                                                                                                                                                                                  The invention provides isolated cDNA molecules coding for spider silk proteins. The spider silk proteins are characterized by repeating alpha and beta regions and optional variable regions. The DNA sequences are useful in the production of spider silk protein by recombinant DNA techniques. The recombinant spider silk proteins may be used for the production of fibers. The present sequence represents the cDNA encoding the spider silk protein 1, derived from the major ampullate gland of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     639 aggtgcaggtgcagcagcagcagcagcagctggaggtgccggacaaggaggactaggtgg 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          totoggatgocogtgocaaggactaccacaagaagaatgagotoctgoagotoctgoago 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agcagcaggtgtcggaggtgttaaagtgggtggagtccgccatccaggcctccaaagttc 753
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                                                                                                                                                                                                            DNA, vector and transformed cell encoding for and useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agcagcagccggaggtgctggacaaggcggatacggtggtcttggtggacaaggtgccgg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2338 BP; 564 A; 432 C; 918 G; 424 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 50.4; DB 21;
Pred. No. 0.01;
0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.clavipes dragline silk protein coding sequence
                                                                                                                                                                                                                             the production of spider silk protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  754 atctgctgtcagcagaccacgaggagga 781
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1..2157
/*tag= a
                                                                                                                                                                                                                                                         Example 3; Fig 6A-D; 65pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.98;
                                                                                                                                      RV;
                                                           91US-0684819
90US-0511792
                               94US-0317844
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                                                                                                                                       Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 132; Conservative
                                                                                                     (UYWY-) UNIV WYOMING
                                                                                                                                                                  WPI; 2000-061225/05.
P-PSDB; AAY59070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                      Xu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nephilia clavipes
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                               04-OCT-1994;
                                                           15-APR-1991;
                                                                          20-APR-1990;
                                                                                                                                      MB,
 23-NOV-1999
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                                                                                                                                       Hinman
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Human; transporter and ion channel-17; TRICH-17; cystic fibrosis; mood; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer; alsease; epilepsy; vaccine; arrhythmis; pick's disease; ischeanic cerebrovascular disease; AIDS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               639 aggigcaggigcagcagcagcagcagcagciggaggigccggacaaggaggactaggigg 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A N.clavipes major ampullate gland cDNA library was screened with probes based on peptide fragments of the purified spider silk protein (see AAQ14185). Positive plaques were identified and the spider silk protein 1 coding sequence was determined. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 tgaagcagtcgcaggtggtcttcgtgctgactgggggactgcggtgaccgcaccctg
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                                                                                                                                                                                                                                                                                                                                                 DNA encoding spider silk protein-1 and 2 and variants - isolated from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        566 A; 433 C; 916 G; 423 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human transporter and ion channel-17 (TRICH-17) cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 47.2; DB 12;
Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches 138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699 acaaggtgctggacaaggagctggagca 726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 23; 48pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.68;
                                                                90US-0511792
91EP-0106217
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Best Local Similarity 48.5
Matches 130; Conservative
                                                                                                                                                                                                Xu M, Hinman
                                                                                                                            (UYWY-) UNIV OF WYOMING
                                                                                                                                                                                                                                                      WPI; 1991-312199/43.
P-PSDB; AAR14308.
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us-09-665-728-2.rng

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muscle disorder; cardiomyopathy; cataract; myocarditis; Grave's disease; dermatomyositis; diabetes mellitus; immunological disorder; psoriasis; rheumatoid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; nootropic; Addison's disease;
 Schizophrenia; polymyositis;
                                   malabsorption syndrome; hypercholesterolaemia; cancer; ss.
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Homo sapiens

/product= "Human TRICH-17 protein' Location/Qualifiers 246..2066

WO200146258-A2.

28-JUN-2001

22-DEC-2000; 2000WO-US35095

14-JAN-2000; 2000US-0176083. 21-JAN-2000; 2000US-0177332. 28-JAN-2000; 2000US-0177332. 02-FEB-2000; 2000US-0179758. 10-FEB-2000; 2000US-0181625.

(INCY-) INCYTE GENOMICS. INC

Lal P; Reddy R, Gandhi AR; Yang J, Yao MG, J, Lu I Nguyen I Au-Young Yue H, Azimzai Y, Hillman JL, Azimz Tang YT, Khan FA; Baughn MR,

WPI; 2001-418042/44.

P-PSDB; AAE04904

Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological disorders

Claim 5; Page 151-152; 160pp; English.

The present sequence is transporter and ion channel-17 (TRICH-17) cDNA.

TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH, such as transport disorder including amyotrophic lateral sclerosis, conditions is. Becker's muscular dystrophy, charcot-Marie Tooth disease, buchene muscular dystrophy, angina and hypertension, neurological disorders including Alzheimer's disease, ammesia, bipolar disease, dementia, depression, epilepsy, ischaemic cerebrovascular disease and Parkinson's disease, but function's disease, Huntington's disease, atroke, cerebral neoplasms, Pick's disease, Huntington's disease and Parkinson's disease, demyelinating disease, Huntington's consisting mood, anxiety, Schizophrenia and seasonal affective disorders, muscle disorder including radiomyopathy, myocarditis, polymyositis, dermatomyositis, arrhythmias and asthma and immunological disorders, anemial disorders and militus, freumatoid arthritis, scleroderma, Sjorren's syndrome, systemic lupus erythematosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary altery stenosis, Grave's disease, Cushing's disease, dinnonary altery stenosis, Grave's disease, Cushing's disease, altery stenosis. glucose-galactose malabsorption syndrome, hypercholesterolaemia, cancers psoriasis and viral, bacterial, fungal, helminthic and protozoal Sections: and Viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic

Sequence 2745 BP; 468 A; 863 C; 822 G; 592 T; 0 other;

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ö
                             Gaps
                          0;
  2745;
   Length
                         Indels
4.2%; Score 43.4; DB 22;
44.3%; Pred. No. 0.5;
                         0; Mismatches 221;
                         Conservative
           Best Local Similarity
Matches 176; Conserv
 Query Match
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The present sequence is human tumour suppressor gene 16 (TSG16). This sequence was isolated from chromosome 16q24.3. TSG16 suppresses cellular proliferation. TSG16 is useful for treating disorders associated with decreased expression or activity of TSG16. e.g. cancers, (auto)immune disorders, inflammation, complications of wound healing and infections
                                                                                                                                                                                        1855 aggaettecagaageaggegtegeeetggeetttgtggggeetgeaggteeeegttetee 1914
                                      tgcgggaggagatcctaagccgggccctggaagtgtccccgccacgctgcttggtcctgg 1794
                                                                                                             1795 agigcacccaigtcigcagcaicgaciacacigiggigcigggacicggagggacicc 1854
                                                                                                                                                                                                                                                                                                                                                 1975 agaagcacctgaggcaggagccagggacccagccctacaacatcagagaagactccattc 2034
                                                                                                                                                                                                                                                                                                                                                                                                                          2035 tggaccaaaaggttgccctgctcaaggcataatggggccacccgtgggcatccacagttt 2094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crawford J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumour suppressor gene 16; TSG16; human; immune response modulator; inflammatory response modulator; signal transduction activator; cytokine inhibitor; gene therapy; anticancer; anti-inflammatory; autioimmune disorder; infection; chromosome 16q24.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid representing the human tumor suppressor gene TSG16, useful e.g. for diagnosis and treatment of tumors, inflammatory and immunological disorders
                                                                                                                                                    571 agotgaagcagtcgcaggtggtcttcgtgctgactggggactgcggtgaccgcacc
  tgagtgtgggggccatcaaggctgccgtggaggttgccaaccccggctccttcatctacg
                                                                       511 tottotoggatgocogtgocaaggactaccacaaagaagaatgagctootgcagctootgo
                                                                                                                                                                                                                                   ctggctacctggcttttgaggagatcgcctccaccagttctggccaagtgttccagctgg
                                                                                                                                                                                                                                                                    1915 gigicotgotgicogotgacotgaaggggitocagiacitototaccotggaagaagcag
                                                                                                                                                                                                                                                                                                              acaagcagcagtgtcggaggtgttaaagtgggtggagtccgccatccaggcctccaaag
                                                                                                                                                                                                                                                                                                                                                                                     751 ttcatctgctgtcagcagaccacgaggaggagggcgaacacatggagaatcccttttg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2095 gcagggtgttccggaaggttcttgtcactgtgattgg 2131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     847
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cellular proliferation suppressor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human tumour suppressor gene, TSG16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH23688 standard; DNA; 9063 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2001-316439/33.
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WPI; 1999-109255/10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence encodes a fusion protein of codon-optimised RAmy3D signal sequence/mature alphal-antitrypsin (AAT). The protein is used
                                                                                                                                                                                                                                                                                                           Protein expression; monocotyledon plant cell; glycosylated antithrombin III; glycosylated alpha I-antitrypsin; AAT; glycosylated antithrombin III; ATI; human serum albumin; HSA; subtilisin BPN'; treatment; emphysema; antithrombotic; blood replacement; ss.
                                                                                                       7943 aacaagtcagtgcgcgaccgtttcaacgcccgccagttcatctcctggctccaggacgtg 8002
                                                                                                                                             8003 gatgacaagtatgaccgcatgaagacttgcctcctcatgcggcagcagcacgaggccgcg 8062
                                                                                     465 atcaaggctgccgtggaggttgccaaccccggctccttcatctacgtcttctcggatgcc 524
                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes
                                                                                                                           (by viruses, bacteria, fungi, parasites, protozoa or helminths).
                                                                                                                                                                                                                                                                                                                                                                                                          /*tag- a
/note- "codon-optimised RAmy3D signal sequence"
76..1260
                                                                  ö
                                                                                                                                                                                                                                                                                          Codon-optimised RAmy3D signal fused to DNA encoding mature AAT.
                                               Length 9063;
                   Sequence 9063 BP; 2492 A; 2546 C; 2654 G; 1371 T; 0 other;
                                                                  Indels
                                                                 67;
                                               22;
                                               Score 41.8; DB Pred. No. 1.7; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 mature AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Pages 34 iii-iv; 53pp; English.
                                                                                                                                                                                    8063 gccctgaacgccgtgcagaggatggagtg 8091
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/note= "encodes
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                                                                                                                                                                                                                                   ВР
                                                                                                                                                                                                                                 AAV41730 standard; DNA; 1260
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97US-0037991.
97US-0038168.
97US-0038169.
                                               Query Match
Best Local Similarity 55.0%;
Matches 82; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-467179/40.
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                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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13-FEB-1997;
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                                                                                                                                                                                                                                                                                                                                                             Synthetic
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producing mature heterologous protein in monocotyledonous plant cells. The method comprises transforming the cells with a chimmert genee comprising a monocotyledon transcription regulator, inducible either during seed maturation or by adding/removing a small molecule, DNA encoding the heterologous protein, and DNA encoding a signal peptide, with the signal peptide causing secretion of the protein from the cell. Proteins expressed in this manner include mature glycosylated alpha increases its serum half-life, mature glycosylated antithrombin III (ATII), mature human serum ablumin (HSA) having the native folding pattern as shown by bilirubin-binding characteristics, or mature active subtilisin BDN. These proteins are useful therapeutically (e.g. AAT for treating emphysema, ATIII as antithrombotic and HSA as blood replacement) or as industrial enzymes (BDN' is used in detergents).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        geacgacateateacgaagtteetggagaacgaggacaggegeteegetageeteeacet 938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          464 catcaaggetgeegtggaggttgeeaaceceggeteetteatetaegtetteteggatge 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
exemplify the invention. The specification describes a method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ccgtgccaaggactaccacaagaagaatgagctcctgcagctcctgcagctgaagcagtc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           644 ttttgaggagatcgcctccaccagttctggccaagtgttccagctggacaagcaggt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cccgaagctgagcatcaccggcacgtacgacctgaagagcgtgctgggccagctgggcat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               caccyccatcttcttcctyccygacyagygcaayctccaycacctygagaacyayctyac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1260 BP; 287 A; 428 C; 350 G; 195 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41.2; DB 19;
Pred. No. 1.4;
0; Mismatches 133;
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79..1497
/*tag= a
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Best Local Similarity 47.6'
Matches 121; Conservative
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us-09-665-728-2.rng

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93WO-US09333.
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                                                           The present sequence encodes a cysteine proteinase isolated from wheat seed (Triticum sp.). The cysteine proteinase is useful for improving gluten for use in the bakery process.
                                                                                                                                                            89 getcageatgaegectagggegeageteetgeegetgeteetggegaeetaeaeagtagt 148
                                                                                                                                                                             336 GTTCAGGTTGTCCCAGAAGGCGCGGAACCGGCGCTCGCGCTCCGGGATGGAGTTGGCGTT 277
                                                                                                                                                                                                99c9gcggcggtcacatctgatgagcccacgaagacgctgtcccccgccacaggagacgc 208
                                                                                                                                                                                                                276 GGGGAGGAGCCCCCCCCCTTCTCGCCAGAAGTCGTAGACGCCCCGGGCCTCCGC 217
                                                                                                                                                                                                                                  209 caccetggcettcgtettcgatgtcaccggctccatgtgggacgatetgatgcaggtgat 268
                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding plant lignin biosynthesis enzymes - used to transform plants to modulate lignin biosynthesis
                                                                                                                                                                                                                                              New DNA coding cysteine proteinase originating from wheat seed useful for improving gluten for use in bakery process
                                                                                                                                              ;
                                                                                                                                                                                                                                                                      269 cgacggcgcctcacgcattctggagcgcagtctgagcagccgcagccgggtca 321
                                                                                                                                                                                                                                                                                      Ouery Match
4.0%; Score 41; DB 20; Length 1747;
Best Local Similarity 48.5%; Pred. No. 1.7;
Matches 113; Conservative 0; Mismatches 120; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                          caffeoyl-CoA 3-0-methyltranferase; lignin;
                                                                                               Sequence 1747 BP; 367 A; 530 C; 522 G; 328 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                        Maize caffeoyl-CoA 3-0-methyltransferase cDNA.
                                           Claim 4; Page 20-22; 29pp; Japanese.
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167..943
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97US-0057082
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                   transgenic plant; ss.
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P-PSDB; AAW89559
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                                                                                                                                                                                                                                                                                                                                                                                                          Maize; corn;
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This DNA sequence encodes a caffeoyl-CoA 3-O-methyltransferase (see AAY05669) of maize. A polynucleotide having this sequence can be amplified from a cDNA library prepared from shoot culture of amplified from a cDNA library prepared from shoot culture of maize line CMA5 using the primars given in AAX25241 and AAX35242. The invention provides methods and compositions relating to altering inspirates and/or the lighin composition of plants.

Solated nucleic acids (see AAX2196-116) that code for proteins (see AAX05657-77) involved in lighin biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells.

AAY05657-77) involved in lighin biosynthesis are claimed. Also claimed nucleic acids can be used to transform a plant to modulate lighin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lighin biosynthesis polynucleotide operably linked to a promoter, growing the plant cell under plant gend of a time sufficient to modulate (preferably increase) lighin biosynthesis in the plant. The plant lighins can be used as chemical feedstock. Plant material of increased lighin content can be used as a fuel source, and in the pulp and paper industry. Decreased lighin content crops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  476 cgtggaggttgccaaccccggctccttcatctacgtcttctcggatgcccgtgccaagga 535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            596 cgtgctgactggggactgcggtgaccgcacccacctggctactggcttttgaggagat 655
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protein transport; cervix cancer; dysplasia; malignancy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1160 BP; 237 A; 417 C; 311 G; 195 T; 0 other;
Claim 2; Page 138-139; 166pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
26..2257
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us-09-665-728-2.rng

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28-JUL-1998 (first entry)
 Homo sapiens.
                                                                                                                                                                                                                       (UYYA ) UNIV
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                                                                                              WO9407522-A.
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                                                                                                                                                                                                                                                                                  The nucleotide and deduced aa sequences of human transducin-like enhancer of split proteins TLE-1 (AAQ62175, AAR51476), TLE-2 (AAQ62176, AAR51477), TLE-3 (AAQ62177, AAR51478) and TLE-4 (AAQ62178, AAR51479), were determined. The aa sequences were compared with that of Drosophila E(spl)m9/10 protein (AAR51481). Comparison of the WD-40 domains of CON motifs of the consensus residues shown in AAR51480. The antigen, human c-myc, human p53, human A-myb and dorsal proteins with respect to nuclear localization site, and casein kinase II and cd2-kinase phosphorylation sites (sequences AAR51482-96). TLE can be used to treat or diagnose (pre)neoplastic conditions, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            230 tgtcaccggctccatgtgggacgatctgatgcaggtgatcgacggcgtctcacgcattct 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLE-2; transducin-like enhancer of split protein; cell fate; differentiation; cervix cancer; breast cancer; psoriasis; baldness;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ggagcgcagtctgagcagccgcagccgggtcatcgccaactatgcgctggtgcctttcca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gcaggtcaccgtgggggggctgaacagcctcatcggggcagcagctccagccgctgtccca
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                                                                                                                                                                       New human transducin-like enhancers of split protein - and. associated multi-protein complexes, chimeric proteins, antibodies, nucleic acid, etc., involved in nuclear-cytoplasmic
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                                                                                              Stifani S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2271 BP; 437 A; 751 C; 672 G; 411 T; 0 other;
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Pred. No. 2.5;
0; Mismatches 141;
                                                                                              Redhead NJ,
                                                                                                                                                                                                                                                       Disclosure; Page 58-61; 112pp; English.
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                                                                                              H111 RE,
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                                            (MEDI-) MEDICAL RES COUNCIL. (UYYA ) UNIV YALE.
              92US-0955011
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Matches 125; Conservative
                                                                                              Artavanis-tsakonas S,
                                                                                                                          WPI; 1994-135597/16.
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The nucleotide and deduced aa sequences of human transducin-like enhancer of split proteins TLE-1 (AAQ45333, AAR51109), TLE-2 (AAQ45334, AAR51111) and TLE-4 (AAQ45335, AAR52953) were determined. The aa sequences were compared with that of Drosophila E(spl) m9/10 (AAR52955). Comparison of the WD-40 domains of these proteins defined the consensus residues shown in AAR22954. The CCN motifs of the proteins were compared with those of SV40 T antigen, human e-myc, human p53, human A-myb and dorsal protein with respect to nuclear localization site, and casalirkinase and cd2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Transducin-like enhancer or split proteins and nucleic acids - are for treatment of disorders of cell fate or differentiation e.g. cervical cancer, breast cancer, psoriasis, baldness etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kinase phosphorylation sites (sequences AAR52956-70).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 40.4; Di
Pred. No. 2.5;
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Location/Qualifiers
26..2257
/*tag= a
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Best Local Similarity 47.0%;
Matches 125; Conservative
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Claim 2; Pages 7-9; 15pp; Japanese.
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97JP-0138461
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                                                        96JP-0184459
                                                                                                             (MIKI-) MIKIMOTO SEIYAKU KK
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Matches 93; Conservative
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(HAST/) HASTINGS G A.
(RUBE/) RUBEN S M.
                                                                                                                                                            WPI; 1998-254410/23.
P-PSDB; AAW56163.
  28-MAY-1997;
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28-AUG-1998;
                                                        15-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New cDNA and e.g. vector, host cell and polypeptide - used to produce polypeptide in high yields, which is used in cosmetics
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                         New DNA sequence isolated from Pinctada fucata.
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                                                                              Pinctada fucata; protein; cosmetic; ds
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                                                                                                                                Pinctada fucata
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The present sequence represents a new DNA sequence isolated from Pinctada fucata. The encoded polypeptide be used as an ingredient in cosmetics.
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New cDNA and e.g. vector, host cell and polypeptide – used to produce polypeptide in high yields, which is used in cosmetics
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                                                                                                                                                                                                                                                                                                                                                                            3.9%; Score 40.2; DB 19;
51.4%; Pred. No. 3.1;
tive 0; Mismatches 88;
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Ruben SM;
Iruela-Arispe L, Hastings GA,
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WPI; 1999-590684/50.

New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders

Disclosure; Page 322-324; 457pp; English

MAZI AAZI 2000 and AAZI 2001 encode, and AAY 49501 and AAY 49502 represent, human metalloprotease thrombospondin (METH) proteins METH1 and METH2.

Tespectively. METH1 and METHZ have been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial venous malformations.

They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, cr mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders may be genetic, somatic, such as toxins), or infectious. They can also be used to treat infiammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAZI2002 to AAZI2080, and AAY49503 to AAY49511 represent sequences given in the exemplification of the present

Sequence 3331 BP; 762 A; 701 C; 1022 G; 846 T; 0 other;

ö 0; Gaps 3.9%; Score 40.2; DB 20; Length 3331; 51.4%; Pred. No. 3.1; tive 0; Mismatches 88; Indels 0; 3.9% Best Local Similarity 51.4% Matches 93; Conservative

553 agctcctgcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctgactggggact 612 766 agccgcagccgctgccgctgcaggaggcgcaggtggacttggaggactcggtggcgg 825 å

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Search completed: March 7, 2002, 21:17:38 Job time: 4551 sec

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March 7, 2002, 20:44:19 ; Search time 1988.65 Seconds
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SUMMARIES

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VDVLVPPAIEGGDETSYFIVMVNNLLELDCHVTGSPPPTIMWLKDGQLIDERDGFKIL
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ISDTGRYTCVAVNAAGEKQRDIDLRVYVPPNIMGEEQNVSVLISQAVELLCQSDAIPP
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BASE COUNT ORIGIN

Gaps ő Length 18207 Score 336.8; DB 9; Length Pred. No. 7e-57; 0; Mismatches 222; Indels 40.8%; Query Match
Best Local Similarity 67.9
Matches .470; Conservative

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- ccacaggagacgccaccctggccttcgtcttcgatgtcaccggctccatgtgggacgatc 160 101 à
- 움
- 161 tgatgcaggtgatcgacggcgcctcacgcattctggagcgcagtctgagcagccgcagcc 220 ô

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 191750)

Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C., Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T., Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T., Buhay,C., Bunac,C., Burket,C., Chacko,J., Chen,G., Chen,Z., Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S., Fernandez,C., Ferraguto,D., Frocum-Tansey,J., Call,R., Gorrell,J.H., Gunzratue,P., Haller,G., Hernandez,J., Hogus,M., Gorrell,J.H., Gunzratue,P., Haller,G., Hernandez,J., Martin,R., Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R., Massey,E., McLeod,M.P., Mei,G., Moore,S., Morgan,M., Morlis,S., Neal,D., Nelson,A., Nuyen,R., Nguyen,N., Oguh,M., Parish,B., Perez,L., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R., Wener,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R. 515 340 575 400 460 695 520 755 580 815 aagtgitccagciggacaagcagcagtgicggaggigttaaagigggiggagiccgcca 640 875 641 tecaggeetecaaagtteatetgetgteageagaceaegaggaggaggagegaacaeae 700 935 AC024113 191750 bp DNA HTG 07-JAN-2001 Mus musculus chromosome 11 clone RP23-277F6, WORKING DRAFT SEQUENCE, 29 unordered pleces. gggtcatcgccaactatgcgctggtgcctttccacgaccagacattggcccagtgaccc gtgactgcccagaaatgagtgtgggggcatcaaggctgccgtggaggttgccaaccccg gtgaccgcacccaccctggctacctggcttttgaggagatcgcctccaccagttctggcc tcacggcggacccagtggtgtttcagagagagctgagacaactctatgttcagggaggtg 576 GTGATTGCCCAGAAATGAGTATTGGAGCTATAAAAATTGCCTTGGAAATTTCTCTTGCTG 756 ATGACAGGACCCATATTGGATATAAAGTCTATGAAGAAATTGCCTCTACAAGTTCTGGTC CAATGATTGAAATTCGCAATCCTTTAGGGAAG 1027 761 ctgagatcgaagtccgggacccactgggtatg 792 AC024113.12 GI:12025591 HTG; HTGS_PHASE1; HTGS_DRAFT. house mouse. DEFINITION ORGANISM 341 966 281 581 221 456 521 ACCESSION VERSION KEYWORDS SOURCE REFERENCE AUTHORS AC024113 TITLE RESULT q q δy g ŏ QQ ολ g ŏ Db òγ g δ g δ a ò à δ

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AF074901 15597 bp mRNA INV 27-FEB-2001
Caenorhabditis elegans hemicentin precursor (him-4) mRNA, complete
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Vogel, B.E. and Hedgecock, E.M.
Hemicentin, a conserved extracellular member of the immunoglobulin
superfamily, organizes epithelial and other cell attachments into
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Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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0; Mismatches 2
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187608: contig of 2571 b
187708: gap of unknown 1
189220: contig of 1512 b
189320: gap of unknown 1
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gap of unknown 1
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gap of unknown 1
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contig of 4168 b
contig of 2655 b
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contig of 1782 b
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gap of unknown
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/chromosome="11"
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Matches 250; Conservative
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Contact: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Center project name: wABS-277F6
Center clone name: RP23-277F6
Center clone name: RP23-277F6
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 74% of reads
Chemistry: Dye-primer Bodipy: 74% of reads
Assembly program: Phrap; version 0.990329
Chemistry: Dye-terminator Big Dye: 26% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155356 bases at least Q30
Consensus quality: 155356 bases at least Q30
Consensus quality: 179582 bases at least Q30
Consensus quality: 179682 bases at least Q30
Consensus quality: 179682 bases; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                Morley, K.C.
Direct Submission
Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Jan 4, 2001 this sequence version replaced gi:11096415.
Center: Baylor College of Medicine
Center: Baylor College of Medicine
Genter: Baylor College of Medicine
Genter: Baylor College of Medicine
Web site: http://www.hgsc.bcm.tmc.edu/
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JOURNAL
                      REFERENCE
                                      AUTHORS
                                                                           JOURNAL
                                                       TITLE
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Gaps

Indels

22;

DB 2; Length 191750;

2835 others

46018 t

240

source

FEATURES

gene

TITLE JOURNAL REFERENCE AUTHORS

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/note="mutants have defects in cell adhesion and germ-line chromosome segregation"
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MYEARERGGTVSRNIPVDKHLSELTISLSGDKDDSDNLDIVLRDPEGRTVDKRLYSKE
GGTIDLKNVKLIRLKDPSPGVWTVNTNSRLKHTIRVFGHGAVDFKYGFASRPLDRIEL
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GKPLQSDKFVKTSANGQKLYLFKLRETDSSKYTCIATNEAGTDKRDFKVSMLVAPSFD
EPNIVRRITVNSGNPSTLHCPAKGSPSPTITWLKDGNAIEPNDRYVFFDAGRQLQISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSMFDDLVQVREGAAKIFKTVMAQREKLIYNYIMVPFHDPYLGEIINTTDSTYFMRQL
SKVYVHGGGDCPEKTLTGILKALQISLPSSFIYVFTDARSKDYHLEDEVLNTIQEKQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FVPPKGLFFVRVQGYDEDNY EFMRTAPTATGSVIVGGPRAFMSPTHQEFVGRDLNLSC
TVESASAYTTYWVKTGEDITGGPLFY HNTDTSVWT I PELSLKDAGEY ECRVISNNGNY
SVKTRVETRESPPETFGVRNVSVPLGEAAFLHCSTRSAGEVETRWTRYGATVFNGPNT
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REGVNLSCEAMGDPK PEVHWY FKGRHLLNDYR Y QVGQDSK FLY I RDATHHDEGTY ECR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AMSQAGQARDTTDLMLATPPKVEIIQNKMMVGRGDRVSFECKTIRGKPHPKIRWFKNG
KDLIKPDDYIKINEGQLHIMGAKDEDAGAYSCVGENMAGKDVQVANLSVGRVPTIIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDQGQFTCIARNTYGQOSQSTTLMVTGLVSPVLGHVPPEEQLIEGQDLTLSCVVVLĞT
PKPSIVWIKDDKPVEEGPTIKIEGGGSLLRLRGGNPKDEGKYTCIAVSPAGNSTLHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQLIKKPEFVYKPEGGIVFKPTISGMDEKHVAVVNSTHDVLDGEGFAIPCVVSGTPPP
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TLTVHEKPKIISEVPGVVDVVKGFTIEIPCRATGVPEVIRTWNKNGIDLKMDEKKFSV
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RVELKCYVEASPPASVTWFRRGIAIGTDTKGYVVESDGTLVIQSASVEDATIYTCKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NPAGKAEANLQVTVIASPDIKDPDVVTQESIKESHPFSLYCPVFSNPLPQISWYLNDK
PLIDDKTSWKTSDDKRKLHVFKAKITDSGVYKCVARNAAGEGGKSFQVEVIVPLNLDE
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ESDDKTTFVWSINGSESDRPDNVQIPSDGHRLYITDAKPENNGKYMCRVTNSAGKAER
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EAVEVNNNHTVVVNNVTKYHTGVYKCYATNKVGQAVKTINVHVRTKPRFESGLTESEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MGRSPSWLYGVLGLLLLATTCSSVNDDKNDPTGKSSLAFVFDIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ARPRPVLNQDTYLLI NMTGLI PPGTVGEI DLVDY HGHSLYKAVA SPHRTNPNMY FAGP
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                                                                                                                                         2 (bases 1 to 15597)
Vogel, B. E. and Hedgecock, E. M.
Direct Submission
Submitted (25-UJW-1998) Biology, Johns Hopkins University, 3400 N.
Charles St., Baltimore, MD 21218, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function="cell adhesion"
/note="alternatively spliced form has been detected"

    1. .15597
    /organism="Caenorhabditis elegans"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone="cosmids F15G9; T09B9"
oriented line-shaped junctions
Development 128 (6), 883-894 (2001)
11222143
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/db_xref="GI:3328186"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6239"
/chromosome="X"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="Bristol N2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="him-4"
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/gene="him-4"
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ö VARVGDTMLLTCNAESSVPLSSVYWHAHDESVQNGVITSKYAANEKTLNVTNIQLDDE GFYYCTAVNEAGITKKFFKLIVIETPYFLDQQKLYPIILGKRLTLDCSATGTPPPTIL FMKDGKRLNESDEVDIJGSTLVIDNPQKEVEGRYTCIAENKAGRSEKDMAVEVLLPPK LSKEWINVEVQAGDPLTLECPIEDTSGVHITWSRQFGKDGQLDMRAQSSSDKSKLYIM YDRYSISPDGSHITINKAKLSDGGKYICRASNEAGTSDIDLILKILVPPKIDKSNIIG NPLAIVARTIYLECPISGIPQPDVIWTKNGMDINMTDSRVILAQNNETFGIENVQVTD QGRYTCTATNRGGKASHDFSLDVLSPPEFDIHGTQPTIKREGDTITLTCPIKLAEDIA DQVMDVSWTKDSRALDGDLTDNVDISDDGRKLTISQASLENAGLYTCIALNRAGEASL RIVEGGQVLQILRTDSDHAĞKWSCVAENDAGVKELEMVLDVFTPPVVSVKSDNPIKAL GETITLFCNASGNPYPQLKWAKGGSLIFDSPDGARISLKGARLDIPHLKKTDVGDYTC QALNAAGTSEASVSVDVLVPPEINRDGIDMSPRLPAQQSLTLQCLAQGKPVPQMRWTL NGTALTHSTPGITVASDSTFIQINNVSLSDKGVYTCYAENVAGSDNLMYNVDVVQAPV ISNGGTKQVIEGELAVIECLVEGYPAPQVSWLRNGNRVETGVQGVRYVTDGRMLTIE VQTIVAPKISTSGNRYINGSEGTETVIKCEIESESSEFSWSKNGVPLLPSNNLIFSED YKLIKTLSTELSDGEPSCTAANKAGNATQKTYLNVGYAPKINERPRTQVVHKGDOVT LWCEASGVPQPAITWYKDHELLINTGODETATTKKKSVIFSSISPSQAGVTCKAENW VASTEEDIDLIVMIPPEVVPERNNVSTNPRQTVPLSCANTGIPEBVISWMEDSNIAIQ APQFIVKPKNTTAAIGAIVELRCSAAGPPHPTITWAKDGKLIEDSKFEIAYSHLKVTL NSTSDSGEYTCMAQNSVGSSTVSAFINVDNNILPTPKPSSNQKNVAVITCYERNQAYS RGLTWEYNGVPMPKNLAGIHFMNNGSLVILDTSSLKEGDLELYTCKVRNRRRHSIPHL TSAFEGVPEVKTIDKVEVNNGDSVVLDCEVTSDPLTTHVVWTKNDQKMLDDDAIYVLP NNSLVLLNVEKYDEGVYKCVASNSIGKAFDDTQLNVYEGDFLPLTGFEGSGINIDDSS MLAIPSGLPISHIATLTAYDKSGRVLNDTTYAISDTGAPLARGRMTSGPFTIKAVKRG /note="48 tandem repeats; Region: immunoglobulin repeats" 14842. .14985 /gene="him-4". ARSLDSGIYLCSATNEAGSAQQAYTLEVLVSPKIITSTPGVLTPSSGSKFSLPCAVRG YPDPIISWTLNGNDIKDGENGHTIGADGTLHIEKAEERHLIYECTAKNDAGADTLEFP NNEKYQILGTTLAIRNVLPDDDGFYHCIAKSDAGGKIATRKLIVNKPSDRPAPIWVEC DEKGKPKKTEYMIDRGDTPDDNPQLLPWKDVEDSSLNGSIAYRCMPGPRSSRTVLLHA RDVNECESVRCEDGKACFNQLGGYECIDDPCPANYSLVDDRYCEPECENCTSTPIQVH QATPEDADSYSCIAVNDAGGAEAVFQVTVNTPPKIFGDSFSTTEIVADTTLEIPCRTE GIPPPEISWFLDGKPILEMPGVTYKQGDLSLRIDNIKPNQEGRYTCVAENKAGRAEQE ILKCPVLGNPTPTVTWKRGDDAVPNDSRHTIVNNYDLKINSVTTEDAGQYSCIAVNEA NAGGSSRREAYKKENEDASTTTITTTSPTTTTTETPLTTTIPALITLPAKQYPTDDY HEGSANDDGFGPTTQDSLFEFNPPLHPEISVVNTDCAGTINENGDCVDKDGKTHNLKI LTGENHCPEGFAMNPHTRICEDLDECAFYQPCDFECINYDGGFQCNCPLGYELAEEGC TYVELSEPPRVVMASEVMRVVEGRQTTIRCEVFGNPEPVVNMLKDGEPYTSDLLQFST KLSYLHLRETTLADGGTYTCLATNKAGESQTTTDVEVLVPPRLEDEERVLQGKEGNTY MVHCQVTGRPVPYVTWKRNGKEIEQFNPVLHIRNATRADEGKYSCIASNEAGTAVADF LIDVFTKPTFETHETTFNIVEGESAKIECKIDGHPKPTISWLKGGRPFNMDNIILSPF GDTLM1LKAQRFDGGLYTCVATNSYGDSEQDFKVNVYTKPY1DET1DQTPKAVAGGE GNLTTHYAAEVIGKPTFVRKGGNLYEVIENDTITMDCGVTSRPLPSISWFRGDKPVYI **EFKVEILSPPVIDISRNDVQPQVAVNQPTIMRCAVTGHPFPSIKWLKNGKEVTDDEN** 99 egecacaggagaegecaccetggeettegtettegatgteaeeggetecatgtgggaega 158 Gaps HAQVWTNRVLAAGDHHKVRVRAHSDHATNELHAPKETNFLVLINVGQYPF' 22.4%; Score 185.2; DB 3; Length 15597; 55.2%; Pred. No. 4.5e-27; ive 0; Mismatches 293; Indels 0; /note="Region: modified EGF repeat" 14986. .15099 /gene="him-4" /note="Region: EGF repeat" 3228 c 3417 g 4003 t EGF repeat" /product="hemicentin" 1300. .14544 /gene="him-4" /note="Region: E 15100. .15228 /gene="him-4" /gene="him-4" 73. .15594 Best_Local Similarity 55.2 Matches 361; Conservative 4949 a misc_feature misc_feature misc_feature misc_feature mat_peptide Query Match BASE COUNT ORIGIN

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Nimberley, A.

Direct Submission

Submitted (16-0402-2011) Sanger Centre, Hinxton, Cambridgeshire,
CBLO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk

on Aug 18, 2001 this sequence version replaced gi:15020463.

During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >-
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL360004 182211 bp DNA PRI 16-AUG-2001
Human DNA sequence from clone RP11-88G17 on chromosome 9, complete
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 182211)
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                                                                                                                                                                                                                                      cctcacggcggacccagtggtgtttcagagagactgagacaactctatgttcagggagg
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                                                                                                                                                                                                                                                                                                                                                         tggtgactgcccagaaatgagtgtggggccatcaaggctgccgtggaggttgccaaccc
                                                                                                                                                                                                                                                                                                                                                                                                             330 AGGTGATTGTCCAGAGACGTTGACCGGTATTCTCAAGGCACTTCAAATTTCCTTACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510 TGGTAATAGAACACATCCAGGATTCCGTACATGAAAAAATCGCGCGCTGCATCTTTGG
                                                      150 TTTGGTGCAAGTACGGGAAGGTGCTGCTAAAATCTTCAAAACTGTGATGGCGCAACGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             getectgeagetectgeagetgaageagtegeagtggtettegtgetgaetggggaetg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 630 TGTCAAACAGAAGAAGTTCATTTGATGTACGAGGCACGTGAACGGGGAGGAACAGTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              570 ACAAGITITICCATCITGAAAAGAGTGATGTCAGTACCGTATTAGAATATGTCAGACATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             699 atggagaatcccttttgaccccagcttgaaggaagtcaccatctcactgagcgg
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AL360004.22 GI:15212049
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abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger.Centre Chromosome 9 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi; mammalla; Eutherla; Rodentla; Sciurognathl; Muridae; Murinae; Mus. 1 (bases 1 to 191750)
Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              constructed by the group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 137369 GCAGTGGCC---GGGGCGCCCGGGACGGTAATGCCCCCCACCACGGGGGACGCCCCTG 137425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 137486 GCCTCGCGCATTCTGGAACGCAGTCTGAGCCGCCGCAGCCAGGCCATCGCCAACTACGCG 137545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Tandem repeat. Forced join. Gap sized to be approximately 150pp from restriction digest data and spanning pUC clone." 40368 a 47059 c 48127 g 46657 t.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus chromosome 11 clone RP23-277F6, WORKING DRAFT SEQUENCE, 29 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 geggteacatetgatgageecacgaagaegetgteecegecacaggagaegecacetg
                                                                                                                                                                                                                                                                                                                            RP11-88G17 The
                                                                                                                                                                                                                                                                                                                                                   right end of clone RP11-202H3 is at 75398 in this sequence
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atgacgectaggggegeageteetgeegetgeteetggegaeetaeaeagtagtggeggeg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcctcacgcattctggagcgcagtctgagcagccgcagccgggtcatcgccaactatgcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           43597. 44209
/note="Sequence from AC006241 sequenced by WIBR".
50279. 50351
/note="Sequence from AC006241 sequenced by WIBR"
93314
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                                                                                                                                                                       Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9
RP11-88G71 is from the library RPCI-11.1 con of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21.5%; Score 177; DB 9; 78.2%; Pred. No. 9.3e-26;
                                                                                                                                                                                                                                                                                                     VECTOR: pBACe3.6
This sequence is the entire insert of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /chromosome="9"
/clone="RP11-88G17"
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Matches 226; Conservative
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KEYWORDS
SOURCE
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Jeduson, D., Thomas, S., Okwuonu, G., Carlock, C., Garner, T.,
Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,
Buhay, C., Bunac, C., Burkett, C., Chacko, J., Chen, G., Chen, S.,
Cox, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S.,
Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R.,
Gorrell, J. H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,
Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S.,
Kovar, C., Liu, J., Liu, W., Loulsegad, H., Lozado, R.J., Martin, R.,
Massey, E., McLeod, M.P., Mel, G., Moore, S., Morgan, M., Morris, S.,
Perez, L., Reiter, D., Say, J., Shen, H., Vasquez, L., Watlington, S.,
Williamson, A., Wrensford, G., Zhou, X., Bouck, J., Hodgson, A.,
Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G.,
Nireat, C., Marian, E., Weinstock, G.,
Nireat, C., Marian, B., Mel, S.,
Norley, K. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chemistry: Dye-primer Bodipy: 74% of reads
Chemistry: Dye-primer Bodipy: 74% of reads
Assembly program: Phrap, version 0.990329
Consensus quality: 175536 bases at least 040
Consensus quality: 173428 bases at least 030
Consensus quality: 176862 bases at least 030
Estimated insert size: 180449; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; agarose-fp estimation
Quality coverage: 3.2x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (24-FEB-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Jan 4, 2001 this sequence version replaced gi:11096415.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 19880 bp in length
gap of unknown length
contig of 18640 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 12371 bp in length
gap of unknown length
contig of 12395 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
of 13270 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of 13079 bp in length
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of 8492 bp in length
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of 8314 bp in length
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of 7213 bp in l
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Contact: hgsc-help@bcm.tmc.edu
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Worley, K.C.
Direct Submission
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AUTHORS
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JOURNAL
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COMMENT

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AC024618 230755 bp DNA HTG 23-SEP-2000
Mus musculus clone RP23-22C1, WORKING DRAFT SEQUENCE, 45 unordered
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Pred. No. 1.3e-24;
0; Mismatches 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="RP23-277F6"
47982 c 47655 g 46018 t
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                                                                                                         3396
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gap of unknown
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gap of unknown
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gap of unknown
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gap of unknown
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/db_xref="taxon:10090"
/chromosome="11"
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Best Local Similarity 90.7
Matches 194; Conservative
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190397
190497
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177871
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189221
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120704 120018: contig of 1/255 bp in length 120019 120119 25200: contig of 5082 bp in length 125201 125300: contig of 5082 bp in length 125301 131332: contig of 6032 bp in length 131331 131432: gap of 100 bp 137931 137931: contig of 6499 bp in length 137932 138031: gap of 100 bp 137932 14638: contig of 6499 bp in length 14639 146438: gap of 100 bp 154168 154267: gap of 100 bp 154168 154267: gap of 100 bp 154261 161318: contig of 7529 bp in length 161319 161418: gap of 100 bp 16467: contig of 7529 bp in length 161319 161418: gap of 100 bp 16467: contig of 6219 bp in length 161319 161418: gap of 100 bp 166637.
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120018: contig of 17255 bp in length
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of 1262 bp in Length
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10629: contig of 1329 bp in length
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26126: contig of 2660 bp in length
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29160: contig of 2934 bp in length
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66324: contig of 3007 bp in length
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86908: contig of 6803 bp in length
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102663: contig of 4875 bp in length
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Mus muscollus, clone RP23-22C1

S barren, B. Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barran, N., Bastien, V., Beda, F., Bodushao, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Campoblano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Collins, J., Caradro, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gyotelte, M., Graham, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Lavine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McRernan, K., McPheeters, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., Murphy, T., Naylor, J., Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Vo'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Trigilio, J., Vossiller, S., Tirrell, A., Travers, M., Trigillio, J., Vossiller, S., Threell, A., Travers, M., Trigillio, J., Vossiller, S., Theodore, J., Tirrell, A., Travers, M., Trigillio, J., Vossiller, S., Challes Street, Cambridge, MA 02141, USA

Nesearch, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using RepeatMasker: html

Http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranlata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentla; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 45 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: 22_C_I

Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 206138 bases at least Q40
Consensus quality: 223560 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: sequence_submissions@genome.wi.mit.edu
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2865 2964: gap of 100 bp
2965 4029: contig of 1065 bp in length
                                                                                                                                                                                                                         Nusbaum, C. and Lander, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seg.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: L5311
                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum
Mus musculus, clone RP23-22C1
                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                 house mouse.
                                                                              SOURCE
ORGANISM
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JOURNAL
                       VERSION
KEYWORDS
ACCESSION
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Direct Summission

Univariated (124-DEC-1994) Nematode Sequencing Project, Sanger Centre, Hinxton, Cambridge CB10 1RQ, England and Department of Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:
jes@sanger.ac.uk or rw@nematode.ustl.edu
Coding sequences below are predicted from computer analysis, using predictions from Genefinder (P. Green, U. Washington), and other available information.

Current sequence finishing criteria for the C. elegans genome current sequence finishing criteria for the C. elegans genome sequencing consortium are that all bases are either sequenced unambiguously on both strands, or on a single strand with both a dye primer and dye terminator reaction, from distinct subclones.

Exceptions are indicated by an explicit note.
IMPORTANT: This sequence is not the entire insert of clone F1569.

It may be shorter because we only sequence overlapping sections once, or longer because we only sequence coverlapping sections neighbouring submissions.

The true left end of clone F1569 is at 1 in this sequence. The true right end of clone F1569 is at 4082 in sequence. The true right end of clone C4303 is at 8835 in this sequence. The start of this sequence (1. .101) overlaps with the end of sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The end of this sequence (41245. .41345) overlaps with the start of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For a graphical representation of this sequence and its analysis see:- http://wormbase.sanger.ac.uk/perl/ace/elegans/seq/sequence?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            join(2873. 3089,3208. 3273,3480. 3823,3869. 3947,4131. 4264)
/gene="F1569.1a"
join(3.33869. 3869,3208. 3273,3480. 3823,3869. 3947,4131. 4264)
/gene="F1569.1a"
                                             20-JUN-2001
                                                                                                                                                                                                                                                                       Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282 (5396), 2012-2018 (1998)
                                                                                                                            HTG; Fibronectin type III repeat; Transfer-RNA; tRNA-Ala.
Caenorhabditis elegans.
Caenorhabditis elegans
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                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 41345)
                                                               Caenorhabditis elegans cosmid F15G9, complete sequence
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141346
/organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
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CDNA EST 9k102e12.5 comes from
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CDNA EST 9k16Bh5.5 comes from
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CDNA EST 9k26694.5 comes from
CDNA EST 9k26522.3 comes from
CDNA EST 9k25222.5 comes from
CDNA EST 9k25222.5 comes from
CDNA EST 9k25222.5 comes from
CDNA EST 9k52222.5 comes from
CDNA EST 9k52223.5 comes from
CDNA EST 9k55223.5 comes from
                                                                                                                                                                                                                                                                                                                                                                        The C.elegans Sequencing Consortium. 2 (bases 1 to 41345)
Sulston, J.E.
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                                             41345 bp
                                                                                                          Z47068.1 GI:634018
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20.8%; Score 171.2; DB 2; Length
Best Local Similarity 90.7%; Pred. No. 1.2e-24;
Matches 194; Conservative 0; Mismatches 18; Indels
                                                                                                 211501 211600: gap of 100 bp 211501 224427 22456: contig of 12826 bp in length 224427 224527; gap of 100 bp 224527 230755: contig of 6229 bp in length. Location/Qualifiers
                  188970 189069: gap of 100 bp 189070 198835: contig of 9766 bp in length 18835: gap of 100 bp 19836: 211500: contig of 12565 bp in length
188969: contig of 10730 bp in length
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2965. .4029
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4130. .5611
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26227. .29160
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33843. .37207
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7077 . 7256,7305 . 7378))
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LLAASTQIRESSPVSSPVKEVSSAASLFANDNGNETERRTPSPTVLNAKKLGGIPWPP
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SE"
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cDNA EST yk55895.5 comes from this gene
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from this gene"
    comes
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llarity 55.6%; Pred. No. 4.2e-12;
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/protein_id="CAB52192.1"
/d_xxef="G1:5701852"
/translation="LGDRDFSRLIDITPASSLSFVLDTTGSMGEEINAAKIQARHLVE
QRRGSPMEPVHYVLVPFHDPGFGPVFTTSDPDSFWQQLNEIHALGGGDEPEMCLSALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thesis (1997) University of Oxford, Department of Biochemistry, MRC Immunochemistry Unit
3 (bases I to 1610)
Snoek, M., Albertella, M.R., van Kooij, M., Wixon, J., van Vugt, H., de Groot, K. and Campbell, R.D.
G7c, a novel gene in the mouse and human major histocompatibility complex class III region, possibly controlling lung tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Localization of eight additional genes in the human major histocompatibility complex, including the gene encoding the casein kinase II beta subunit (CSNKZB) Genomics 36 (2), 240-251 (1996)
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Albertella, M.R., Jones, H., Thomson, W., Olavesen, M.G. and Campbell, R.D.
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                                                                                 15883 GAACGGGGAGGAACAGTGTCTAGAAACATCCCAGTAGACAAGCATCTCTCAGAGCTCACC 15942
                              15763 ATCGCCGCTGCATCTTTTGGACAAGTTTTCCATCTTGAAAAGAGTGATGTCAGTACCGTA 15822
                                                               678
atcycctccaccagttctggccaagtgttccagctggacaagcagcagtgtcggaggtg 618
                                                                                                                                   Direct Submission
Submitted (02-AUG-1999) Aguado B., HGMP Resource Centre, MRC,
Genome Campus, Hinxton, Cambridge, CB10 1SB, UNITED KINGDOM
Location/Qualifiers
                                                                 619 ttaaagtgggtggagtccgccatccaggcctccaaagttcatctgctgtcagcagaccac
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/db_xref="taxon:9606"
/chromosome="6"
/map="6p21.3"
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G7c gene; G7c protein.
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Albertella, M.R.
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Molecular analysis of the major MHC recombinational hot spot
located within the G7c gene of the murine class III region that is
involved in disease susceptibility
J. Immunol. 160 (1), 266-272 (1998)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
1 (bases 1 to 4312)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 atgtgggacgatctgatgcaggtgatcgacggcgcctcacgcattctggagcgcagtctg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aagaagaatgagctcctgcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctg
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                                                                                                                                                                                                                                                                                                                                      Length 1610;
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                                                                                                                                                                                                                                                                                                                                      Score 93.6; DB 9;
Pred. No. 8.2e-09;
0; Mismatches 199;
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52.8%;
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                                                                      Submitted (12-MAR-1999) Molecular Genetics, the Netherlands Cancer Institute, Plesmanlaan 121, Amsterdam 1066 CX, The Netherlands Location/Qualifiers
                                                                                                                                                                                                                                  /gene-"G7c"
/note="D17H6S56E-3; genomic structure of the G7c gene is
presented in GenBank Accession Number AF134318; similar t
the human sequence in GenBank Accession Number AJ245418"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="exons around recombinational hot spot; corresponds to sequence presented in Genbank Accession Number
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1243 GGCAGCCCCAT---GGAGCCTGTTTCTATATCCTAGTGCCCTTCCACGACCCAGGGTTT 1299
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                                         Snoek H., Van Kooij, A., van Vugt, H. and de Groot, K.E. Direct Submission
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                                                                                                                               /organism="Mus musculus"
/strain="BALB/c"
/db_xxef="Laxon:10090"
/chromosome="17"
/map="19.00 cM; between G7a and G7"
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Immunogenetics 51 (4-5), 383-386 (2000)
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/protein_id-"AAF61401.1"
/db_xref-"G1:7381105"
                                                                                                                                                                                                        /tissue_type="brain"
1. .4312
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                              (bases 1 to 4312)
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/gene="G7c"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AL135796 157029 bp DNA PRI 27-SEP-2000
Human DNA sequence from clone GS1-164L12 on chromosome 1 Contains
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                   1360 GCCTTGGGGGGTGGAGATGAGCCAGAGATGTGCCTGTCTGCCCTGGAGCTAGCCTGTTG 1419
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GS1-164L12 is from the library Genome_Systems_ReleaseI VECTOR;
pBeloBAC11
This sequence is the entire insert of clone GS1-164L12 The true
left end of clone GS1-15303 is at 103097 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1480 CTTACCAACCGGGTGGAATCCCTGACTCGGGAGGGGGCGCTGCAGGGTGACATTTCTAGTA 1539
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/note="LlME2 repeat: matches 5602. .6150 of consensus"
328 gitcagggaggiggigacigcccagaaaigagiggggggccaicaaggcigccgiggag 387
                                                                                                                                                                                          gttgccaaccccggctccttcatctacgtcttctcggatgcccgtgccaaggactaccac
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1064. .1512
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/db_xref="taxon:9606"
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Donnelly, S.
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| 100te="Alludo repeat: matches 27. 287 of consensus" |
| 13992. | 14992 |
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| 14993. | 15642 |
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| 1668. | 15818 |
| 16688. | 1673 |
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/note="AluJb repeat: matches 148. .289 of consensus"
26950. .26985
/note="18 copies 2 mer tg 97% conserved"
26952. .26987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164. .7191

'note="7 copies 4 mer ttat 96% conserved"

1500. .7576

'note="12 repeat: matches 2645. .2739 of consensus"
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"note="AluSq repeat: matches 1. .308 of consensus"
1440. .9901
"note="MLTID repeat: matches 1. .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .218 of consensus"
                                                                                                                                                                                                                                                                                     435. 3488
note="27 copies 2 mer tg 88% conserved"
119. 4244
note="MiR repeat: matches 23. .152 of consensus"
                                                                                                                                                                                                        3434. .3489
/note="14_copies 4 mer gtgt 87%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  902. .7098
note="MER20 repeat: matches 8.
complement(2521. .2710)
/note="match: GSS: Em:AQ761942"
2792. .3250
                                                                                                                          792. .3250
note="match: GSS: Em:AQ246643"
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/note="MIR repeat: matches 20. .141 of consensus"
/135. .41618
/135. .41618
/135. .41618
/135. .41618
/135. .41618
/135. .41618
/1350. .4344
/note="Anux repeat: matches 19. .307 of consensus"
/note="Limbo repeat: matches 1211. .1677 of consensus"
/1363. .44142
/note="Limbo repeat: matches 2530. .3129 of consensus"
/1353. .45571
/note="Anuxb repeat: matches 3. .41 of consensus"
/5533. .45571
/note="Aluxb repeat: matches 3. .41 of consensus"
/15504. .46529
/note="Limba repeat: matches 4758. .6124 of consensus"
/13630. .47199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(51651. .52071)
/note="match: GSS: Em:AQ636105"
52290. .52512
/note="Liph15 repeat: matches 5785. .6156 of consensus"
53936. .53296
/note="Liph15 repeat: matches 5785. .6156 of consensus"
53335. .53350
/note="7 copies 4 mer gtgt 96% conserved"
53355. .53457
/note="Liph15 repeat: matches 5689. .5791 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="match: STS: Em:G37800"
38212. .38679
/note="LIMC1 repeat: matches 5847. .6324 of consensus"
40470. .40593
/note="MIR repeat: matches 8. .140 of consensus"
41014. .41123
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/note="MBR45B repeat: matches 199. .318 of consensus"
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                                                                                                                                                                                                                                                                                                        73.05 of consensus"
33.363. .33795
7.00te="L2 repeat: matches 2562. .2690 of consensus"
7.00te="L2 repeat: matches 2250. .2690 of consensus"
7.00te="AluSq repeat: matches 18. .297 of consensus"
7.00te="match: GSS: Em:AQS67379"
7.319. .37339
/note="9 copies 4 mer tgtg 97% conserved"
27687. .27917
/note="AluJo repeat: matches 83, .304 of consensus"
29345. .29476
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/note="108 copies 2 mer tt 57% conserved"
complement(54152. ,54622)
                                                                                                                 .2750 of
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                                                                                                 complement(54152. .54622)
/note="match: GSS: Em:AQ568896"
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Human DNA sequence from clone GS1-118G19 on chromosome 1q25.1-31.1,
Complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      important: This sequence is not the entire insert of clone $$1-118619 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone $$31-204112$ is at $$352$ in this sequence. The true right end of clone $$31-204112$ is at $$100$ in this sequence. Location/Qualifiers $$1.804112$ is at $$100$ in this sequence. In $$17461$
                                                                                                                                                                                                                                                                                                         Db 125632 AGGTATTAAAATGGGTAGAAGGAGGAGTACAGGCCTCCAAAGTTCACCTTTTATCCACAG 125691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Db 125752 TCACTGTGTCTTTGAGTGGGCCCTTCTCCAATGATTGAAATTCGCAATCCTTTAGGTGAGA 125811
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87461)
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                                                                                          Length 157029;
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                                                                                                                                                                                    ,92
                                                                                     Query Match 10.8%; Score 89.4; DB 9; Best Local Similarity 64.0%; Pred. No. 1.6e-08; Matches 135; Conservative 0; Mismatches 76;
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54340. .54856
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// Note="WLTIC repeat: matches 2. .466 of consensus" | 1084. .11020 | 1084. .11020 | 1084. .11020 | 1084. .11020 | 1084. .11020 | 1084. .11020 | 1084. .11020 | 1086. .13925 | 10926. .13925 | 10926. .13952 | 10926. .13952 | 10926. .13952 | 10926. .13952 | 10926. .13952 | 10926. .13952 | 10926. .13952 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .1727 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 10926. .18002 | 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Sequence confirmed by AC023275 sequenced by WUGSC" 6728. 6926
/note="NIR repeat: matches 56. .259 of consensus" 7074. 7136
/note="MIR repeat: matches 50. .112 of consensus" 8362. 8848
/note="MIR3D repeat: matches 6. .459 of consensus" 10408. .10856
/note="MIR3D repeat: matches 5. .466 of consensus" 106086
/note="MIR3D repeat: matches 5. .466 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                              2110. 2157
/note="24 copies 2 mer gt 95% conserved"
2166. 2326
/note="4luSg/x repeat: matches 149. 309 of consensus"
2329. 2936
/note="LIMA9 repeat: matches 5177. 5779 of consensus"
2936. 3566
/note="LIMA9 repeat: matches 4500. 5146 of consensus"
3794. 3891
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/note="MBR5A repeat: matches 13. 112 of consensus"
/note="MIR repeat: matches 59. 247 of consensus"
complement(5905. 5949)
                                                                                                                                                                                        568. .694
/note="L2 repeat: matches 2572. .2706 of consensus"
                                                                                                                                                                                                                                                                                         .2748 of consensus"
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26376. .26824
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                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Genome_Systems_ReleaseI"
                                                                                                                     5. .571
/note="L2 repeat: matches 2120.
                                                                                                                                                                                                                                                                                     'note="AluJo repeat: matches 1.
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/note-"MIR repeat: matches 2.
23750. .23852
                                                        /clone="GS1-118G19"
/chromosome="1
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repeat_region

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JOUNCE—"MIR repeat: matches 196. .260 of consensus" 30908. .30959

//note="MIR repeat: matches 82. .140 of consensus" 32916. .32938

//note="MIR repeat: matches 17. .142 of consensus" 33149. .33494
//note="Lizer repeat: matches 17. .142 of consensus" 33149. .33613
//note="Lizer repeat: matches 2355. .2710 of consensus" 35619. .36148
//note="Lizer repeat: matches 183. .1570 of consensus" 35619. .3644
//note="Mir repeat: matches 1635. .2727 of consensus" 36434. .36607
//note="Mir repeat: matches 15. .312 of consensus" 40801. .41093
//note="Lizer repeat: matches 5745. .6173 of consensus" 42231. .42360
//note="Lizer repeat: matches 5721. .6157 of consensus" 42231. .42360
//note="Lizer repeat: matches 1880. .2750 of consensus" 42230. .44137
//note="Lizer repeat: matches 1880. .2750 of consensus" 44684. .44580
//note="Mir repeat: matches 1880. .2750 of consensus" 44684. .44580
//note="Mir repeat: matches 178. .426 of consensus" 44684. .44584
//note="Mir repeat: matches 57.311 of consensus" 44684. .44584
//note="Mir repeat: matches 178. .426 of consensus" 44684. .44584
//note="Mir repeat: matches 1247. .1880 of consensus" 46881. .45514
//note="Lizer repeat: matches 1247. .1880 of consensus" 46881. .45813. .46812. .45814
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/#046="L2 repeat: matches 1235. 1662 of consensus" 49871. 49964
/#046="MIR repeat: matches 20. .127 of consensus" 49931. 50252
/#046="MIR repeat: matches 173. .456 of consensus" 50253. 50564
/#046="MIR repeat: matches 173. .456 of consensus" 50253. 50564
/#046="MIRT repeat: matches 1. .312 of consensus" 50565. .50748
/#046="MIRT repeat: matches 1. .173 of consensus" 50981. .51277
/#046="MIRT repeat: matches 1. .296 of consensus" 50981. .5177
/#046="Alux repeat: matches 1. .296 of consensus" 51693. .51718
        repeat: matches 6536. .6597 of consensus'
29391. .29470
"hote-"FLAM_A repeat: matches 42. .121 of consensus"
19472. .29787
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700c="L2 repeat: matches 1729. .2035 of consensus"

53456. .53885

7note="L2 repeat: matches 2285. .2730 of consensus"
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47636. .47950
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                                                                                                          Joseph 2016, 2016, 2 mer at 78% conserved" 30307. 30453 mer at 78% conserved" 30307. 30453 matches 79. 213 of consensus" 30455. 30751 matches 1. 297 of consensus" 30775. 30836
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48164. .48425
/note="L2 repeat: matches 2431. .2710 of consensus
48443. .48632
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/note="13 copies 2 mer tt 100% conserved"
5.2126. .52507
/note="MIR repeat: matches 76. .244 of consensus"
5.258. .52629
/note="MIR repeat: matches 75. .149 of consensus"
5.2640. .52807
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Direct Submission
Submitted (09-MAY-2001) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Aug 17, 2000 this sequence version replaced gi:7630968.
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4444 Forest Park Parkway, St. Louis,
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Eukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 18024)

Sulston, J.E. and Waterston, R.

Sulston, J.E. and Waterston, R.

Genome Res. 8 (11), 1097-1108 (1998).
                                                                                                                                                                                                                                                                                                                         Department of Genetics, Washington
Park Avenue, St. Louis, Missouri 63108,
                                                                                                                                                                                                                101 ccacaggagacgccaccctggccttcgtcttcgatgtcaccggctccatgtgggacgatc 160
                                                                                                                                                                                                                                                                                              161 tgatgcaggtgatcgacggcctcacgcattctggagcgcagtctgagcagcagccgcagcc 220
54316. .54481

/note="83 copies 2 mer tt 56% conserved"

55309. .55565

/note="Libb repeat: matches 1211. .1474 of consensus"

56353. .56011

/note="Lib4 repeat: matches 3491. .4067 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC023275 180248 bp DNA PRI 09-MAY-2001
Homo sapiens BAC clone RP11-375L10 from 1, complete sequence.
AC023275
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Submitted (17-AUG-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
Mo 63108, USA
5 (bases 1 to 180248)
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                                                                                                                                   Query Match 8.5%; Score 69.8; DB 9; Length 87461; Best Local Similarity 63.3%; Pred. No. 0.00013; Matches 107; Conservative 0; Mismatches 62; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                          Swearengen, S., Maupin, R., Drone, K. and Gregory, S. The sequence of Homo sapiens BAC clone RP11-375L10 Unpublished
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Direct Submission
Submitted (10-SEP-2000) Genome
University School of Medicine,
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Waterston, R.
Direct Submission
Submitted (08-NOV-2000) De
University, 4444 Forest P7
(bases 1 to 180248)
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Waterston, R.H.
Direct Submission
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Waterston, R.H.
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EST W86641 (NID:91400389) zh63e05.s1"
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/rpt_famly_L1

20558. 21137

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22114. 22331

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34177. 34516
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27270. 2726
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28124. 2838
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29167. 29275
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30495. 30677
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31025. 31217
7.rpt_family="MIR"
32939. 33406
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36643. 36920
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36969. 37038
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/rpt_family="L1"
23004. .23307
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10000. .30223
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3740. .24219
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6047, 2610
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/rpt_family="
18161. .18263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute
                                                                                                                                                            NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VECTOR: pBACe3.6
NEIGHBORING SEQUENCE INFORMATION:
Actual start of this clone is at base position 1 of RP11-375L10;
actual end is at base position 180248 of RP11-375L10.
Location/Qualifiers
               Center: Washington University Genome Sequencing Center
                                Center code: WūGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson wustl.edu
Summary Statistics
                                                                                         Center project name: H_NH0375L10
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/chromosome="1"
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/rpt_family*"MER1_type"
3685. .9728
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VECTOR: pBACe3.6
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567. .820
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5140. 5262

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6076. 6593

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6767. 7258
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8958. .9011
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12246. 12330
/rpt_family="MIR"
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rpt_family="L1"
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STS from H.sapiens random shear fragment, sequence tagged site.
AL159308
AL159308.1 GI:7210622
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/tissue_type="Lymphoblastoid cell line"
/clone_lib="SC9-12pJ"
1 198 c 211 g 120 t 2 othe
                                                                                                   8.5%; Score 69.8; DB 9;
63.3%; Pred. No. 0.00011;
tive 0; Mismatches 62;
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/db_xref="taxon:9606"
/chromosome="9"
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43701. 43931
/rpt_family="Alu"
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/rpt_family="Alu"
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Best Local Similarity 72.4%;
Matches 84; Conservative (
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                                                                                                                            Matches 107; Conservative
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Chases 1 to 356)
Dib,C., Faure,S., Fizames,C., Samson,D., Drouot,N., Vignal,A., Millasseau,P., Marc,S., Hazan,J., Seboun,E., Lathrop,M., Gyapay,G., Morissette,J. and Weissenbach,J.
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                                                                                                                         STS; CA repeat; dinucleotide repeat; GT repeat; microsatellite DNA; microsatellite marker; repeat polymorphism.
                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (01-SEP-1995) Genethon, B.P. 60, 91002 Evry Cedex France.
E-mail: Jean.Weissenbach@genethon.fr
                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 356)
Weissenbach,J.
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HS348TG1 356 bp DNA STS 22-MAR-1996 H.sapiens (DIS2848) DNA segment containing (CA) repeat; clone AFM348tg1; single read, sequence tagged site.
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/chromosome="1"
/cell_line="cEPH 134702"
/clone_lib="genomic DNA"
/note="cloning vector is M13mp18"
/note="cloning vector is M13mp18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 7.5%; Score 61.6; DB 11; Best Local Similarity 68.7%; Pred. No. 0.024; Matches 79; Conservative 0; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:9606"
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/organism="Homo
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Rattus norvegicus.
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                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            930621 seqs, 428662619 residues
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Gapop 10.0 , Gapext 1.0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/*tag= a /product= "Rat secreted factor" 96..158

q /*tag= b 159..923 /*tag= c 27-SEP-2000; 2000WO-US26582.

WO200123419-A2

05-APR-2001.

mat_peptide

sig_peptide

99US-0156277.

27-SEP-1999;

(SCIO-) SCIOS INC

Location/Qualifiers

Key

SUMMARIES	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	64 Rat cDNA clone P00					Himan transporter				To Time Time 2 dene	
SUMIN	A		AAF824	AAT853	AAV232	AA2381	AA0141	AAD09568	AAH236	AAV417	AAX252	AA062176	AAOAF3
	DB		7.7	18	19	21	12	22	22	19	20	15	5
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ď	Query Match		100.0	6.3	6.1	6.1	5.7	5.3	5.1	5.0	4.9	4.9	6.4
	Score		972	51.6	50.4	50.4	47.2	43.4	41.8	41.2	40.8	40.4	40.4
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	13	40.2	4.9	2214	19	AAV22682	New DNA segmence i
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	C ;	40.7		3331	77	AAC90078	D86074 cDNA clone.
	16	39.6	٠.	2502	16	AAQ80752	DNA-polymerase con
	17	39.6	•	2502	19	AAV65782	Thermus DNA polyme
	18	39.6	•	2502	20	AAV63403	Consensus DNA sequ
ပ	19	39.4	•	4748	22	AAD06573	Bovine alphal(I) c
	20	38.8	•	1929	19	AAV57472	Sorghum bicolor (L
	21	38.8	•	2668	21	AAD00337	Wheat raffinose sy
	22	38.6	•	1598	14	AAQ40461	E.coli mdh promote
	23	38.2	٠	1995	13	AAQ14184	N.clavipes draglin
	24	38.2	•	1995	19	AAV23250	Nephila clavipes s
	52	38.2	٠	1995	21	AAZ38196	N. clavipes spider
	56	38	٠	1588	22	AAH26304	Spider silk protei
U	27	37.8	٠	1747	70	AAV82459	Triticum sp. cyste
	28	37.6	4.6	267	21	AAA29550	HIV codon altered
ပ	59	37.4	•	571	20	AAV89296	EST clone CH227.
Ç	30	37.4	4.5	31.20	21	AAA12510	encoding a
Ç	31	37.4	4.5	5145	21	AAC98196	Human colon cancer
	32	37.4	•	6085	18	AAT70153	S.longisporoflavus
	33	37.4		31422	21	AAA92302	S. avermitilis ave
O	34	37.2	٠	355	21	AAC74463	Human ORFX ORF18 p
	35	37.2		5335	21	AAC66076	
	36	37	•	2000	18	AAT66543	50K-cellulase B de
	37	37		42000	21	4	Streptomyces alobi
	38	37		63164	21	AAA63348	
ပ	39		•	1886	20	AAZ32026	-
O	40		4.5	1886	22	AAC90083	
O	41	36.8	4.5	24379	18	AAT93095	· C
O	42			4	19	AAV25925	
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RES	RESULT	-					
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The present sequence encodes a novel secreted factor. The invention relates to a polypeptide comprising a sequence of at least 80% identity to residues 22-122 of a 275 amino acid sequence, or a sequence encoded by a nucleic acid hybridising under stringent conditions to the complement of the coding region comprising 1031 nucleotides, and having at least one biological activity of the polypeptide encoded by clone P00210009. The polypeptides and polynucleotides of the invention are useful for the treatment of cardiac, renal and inflammatory diseases. The polypucides are useful in antisense mediated gene inhibition and in gene therapy. The polypeptides are useful in assays for identifying lead compounds that may be useful in assays for
                                                                                                                           Novel secreted factor encoded by clone P00210D09 useful for diagnosing, treating and/or preventing various cardiac, renal and inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           treatment of cardiac, kidney or inflammatory diseases.
                                                                                                                                                                                                                    Claim 1; Fig 2; 69pp; English.
                      Kapoun AM;
                                                           WPI; 2001-328177/34
                                                                                    P-PSDB; AAB83147
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                      Stanton
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Sequence 1031 BP; 215 A; 317 C; 308 G; 191 T; 0 other;

; 0 480 goggicacaictgaigageceaegaagaegeigteeeeegeeaeagaagaegeeeetg 120 215 gccttcgtcttcgatgtcaccggctccatgtgggacgatctgatgcaggtgatcgacggc 180 216 goottogtottogatgtoaccggotcoatgtgggacgatotgatgcaggtgatcgacggc 275 240 335 gigggggccaicaaggcigccgiggaggitgccaaccccggciccitcaictacgictic 420 515 575 96 atgacgoctagggcgcagotcctgccgctgctcctggcgacctacacagtagtggcggcg 155 tttcagagagagctgagacaactctatgttcagggaggtggtgactgcccagaaatgagt 360 Gaps 9 gectcaegeattetggagegeagtetgageageegeageeggggteategeeaaetatgeg 1 atgacgectagggcgcageteetgeegetgeteetggcgacetacacagtagtggcggcg goctcacgcattctggagcgcagtctgagcagccgcagccgggtcatcgccaactatgcg ; Query Match
Best Local Similarity 100.0%; Pred. No. 8e-187;
Matches 825; Conservative 0; Mismatches 0; Indels 0: 336 61 181 276 241 301 396 361 456 516 121 421 셤 q 셤 g ò g ò g à a ò g ò ò ò ò

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601 cagcaggtgtcggaggtgttaaagtgggtggagtccgccatccaggcctccaaagttcat 660

tacctggcttttgaggagatcgcctccaccagttctggccaagtgttccagctggacaag

900

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concoling silk process involves: (a) selecting target DNA, encoding silk protein. The process involves: (a) selecting target DNA, from a silk-producing spider, that contains many repetitive and non-repetitive regions; (b) selecting a single-stranded DNA primer of at least 10 nucleotides, with a sequence that is complementary to a region of the target; (c) repetitively combining the primer with melted target DNA, incubating the mixture with nucleotides and a DNA polymerase with profreading activity to produce a DNA fragment which is complementary to the target and is at least 2 kb long. The present sequence represents a 2 kb DNA sequence which encodes the spider silk protein from Nephila clavipes. The DNA fragment can be used to make fibres, from Nephila clavipes. The DNA fragment can be used to make fibres, and absorbers (e.g. of heavy metals, biological weapons, DNA, chemicals, concerns and fragrances). The high molecular weight (90-250 kD) of
ctgctgtcagcagaccacgaggaggaggcgaacacacatggagaatcccttttgaccc
                                                              agettgaaggaagteaceateteaetgagegggeeagggeetgaagategggae
                                                                                                                                            816 agcttgaaggaagtcaccatctcactgagcgggccagggcctgagatcgaagtccgggac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New opt. multimerised DNA sequences encoding spider silk protein contg. both repetitive and non-repetitive sequences, useful for making high strength films, fibres, woven articles etc.
                                                                                                                                                                                                                                                                                                                                                                                                                High strength film; fibre; woven article; parachutes; sails; absorber; body armour; heavy metal; biological weapon; chemical; flavour; fragrance; Nephila clavipes; ss.
                                                                                                                                                                                                                                                                                                                                                                                       Nephila clavipes spider silk protein 2 Kb DNA sequence.
                                                                                                                                                                          /product Silk_protein
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/*tag= a
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ELION G R.
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Example 3; Column 25-30; 68pp; English
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                                                                                                                                                              Best Local Similarity 49.3
Matches 132; Conservative
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P-PSDB; AAY59070.
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                                                                                                   and elasticity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Nephila clavipes; silk protein; tandem repeat; fibre; dragline;
tensile strength; elasticity; ss.
spider silk proteins can be produced on a commercial scale (at over 2 g/l cell mass). It has better tensile strength and elasticity than silkworm silk. Inclusion of both repetitive and non-repetitive regions ensures isolation of stable clones.
                                                                                                                                                                                   1274
                                                                                                                                         1155 tcttggaagccaaggtgcaggacgaggtggattaggtggacaaggtgcaggtgcagcagc 1214
                                                                                                                                                                                                                        1275 acaaggaggctatggaggacttggaagccaaggttctggtcgaggaggattaggtggaca 1334
                                                                                                                                                                                                                                                                  1335 aggtgcaggtgcagcagcagcagcagctggaggtgctggacaaggaggattaggtggaca 1394
                                                                                                                       teteggatgeeegtgeeaaggaetaeeaaagaagaatgageteetgeageteetgeage 478
                                                                                                    Gaps
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                                                                                                                                                                                                      gctacctggcttttgaggagatcgcctccaccagttctggccaagtgttccagctggaca
                                                                                                                                                                                                                                               agcagcagtgtcggaggtgttaaagtgggtggagtccgccatccaggcctccaaagttc
                                                                                                   ó,
                                                                                Length 2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant spider silk proteins - useful for making fibres
                                                 Sequence 2004 BP; 481 A; 386 C; 791 G; 346 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                        Nephila clavipes spider silk protein encoding cDNA
                                                                         6.3%; Score . 0.0047; 49.6%; Pred. No. 0.0047; ... 0; Mismatches 134; ... 0; Mismatches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product= "spider silk protein 1"
                                                                                                                                                                                                                                                                                                          1395 aggtgctggacaaggagctggagcag 1420
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90US-0511792.
94US-0317844.
95US-0425069.
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                                                                                       Best Local Similarity 49.6
Matches 132; Conservative
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/*tag=
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20-APR-1990;
04-OCT-1994;
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                                                                                Query Match
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The present sequence encodes a spider silk protein from the present invention. Spider silk proteins, and peptide fragments within the proteins, can be produced and purified independently and can then be mixed and made into fibres that have higher tensile strengths and elasticity than naturally occurring fibres. The fibres can be used in mixed composites. The invention allows the two naturally occurring Nephila clavipes silk proteins to be produced independently so that they can later be combined to form silk fibres of high tensile strength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           teteggatgecegtgecaaggaetaceacaagaagaatgageteetgeageteetgeage 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 50.4; DB 19;
Pred. No. 0.0088;
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                                   proteins. The spider silk proteins are characterized by repeating alpha and beta regions and optional variable regions. The DNA sequences are useful in the production of spider silk protein by recombinant DNA techniques. The recombinant spider silk proteins may be used for the production of fibers. The present sequence represents the cDNA encoding the spider silk protein 1, derived from the major ampullate gland of
                             invention provides isolated cDNA molecules coding for spider silk
                                                                                                                                                                                      tctcggatgcccgtgccaaggactaccacaagaagaatgagctcctgcagctcctgcagc 478
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                                                                                                                                                                    Indels
                                                                                                                 Sequence 2338 BP; 564 A; 432 C; 918 G; 424 T; 0 other;
                                                                                                                                               Score 50.4; DB 21;
Pred. No. 0.0088;
0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N. clavipes dragline silk protein coding sequence.
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        6A-D; 65pp; English.
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                                                                                                                                               6.18;
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Best Local Similarity 49.3
Matches 132; Conservative
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                                                                                                Nephila clavipes
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       3; F1g
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Human; transporter and ion channel-17; TRICH-17; cystic fibrosis; mood; gene therapy; amyotrophic lateral sclerosis; amnesia; muscular dystrophy; hypertension; angina; neurological disorder; asthma; bipolar disorder; dementia; depression; Alzheimer's disease; epilepsy; vaccine; arrhythmia; pick's disease; ischaemic cerebrovascular disease, AlDS; anxiety; stroke; Huntington's disease; Parkinson's disease; cerebral neoplasm; allergy; demyelinating disease; mental disorder; Schizophrenia; polymyositis; muscle disorder; cardiomyopathy; cataract; myocarditis; diabetes mellitus; immunological disorder; psoriasis; rheumatooid arthritis; Sjogren's syndrome; systemic lupus erythematosus; sickle cell anaemia; Wilson's disease; infertility; Cushing's disease; scleroderma; pulmonary artery stenosis; notropic; Addison's disease; malabsorption syndrome; hypercholesterolaemia; cancer; ss.
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                                                                                                                                                                                                             A N.clavipes major ampullate gland cDNA library was screened with probes based on peptide fragments of the purified spider silk protein (see AAQ14185). Positive plaques were identified and the spider silk protein I coding sequence was determined. See also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          519 agcagcagccggaggtgctggacaaggcggatacggtggtcttggtggacaaggtgccgg
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       - isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2338;
DNA encoding spider silk protein-1 and 2 and variants - isola from Nephila clavipes, for prodn. of spider silk protein and fibres having desired characteristics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence 2338 BP; 566 A; 433 C; 916 G; 423 T; 0 other;
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/product= "Human TRICH-17 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47.2; DB 12;
Pred. No. 0.051;
0; Mismatches 138;
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246..2066
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                                                                                                                                      Claim 4; Page 23; 48pp; English.
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Best Local Similarity 48.5%;
Matches 130; Conservative (
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The present sequence is transporter and ion channel-17 (TRICH-17) cDNA.

TRICH is used as vaccine. TRICH is useful for treating a disease or condition associated with decreased expression of functional TRICH.

Such as transport disorder including amyotrophic lateral sclerosis, cystic fibrosis, Becker's muscular dystrophy, Charcot-Marie Tooth disease.

CC disease, Duchenne muscular dystrophy, angina and hypertension, churchogical disorders including Alzheimer's disease, mensia, bipolar disease, stroke, cerebral neoplasms, Pick's disease, Huntington's disease and Parkinson's disease, demyelinating diseases, mental disorders including mood, anxiety, Schizophrenia and seasonal affective disorder, dermatomyositis, arrhythmias and asthma and immunological disorder; dermatomyositis, arrhythmias and each and infamon and asthma and immunological disorder; concluding AIDS, adult respiratory distress syndrome (ARDS), allergies, sincluding AIDS, adult respiratory distress syndrome (ARDS), allergies, sanemia, diabetes mellitus, rheumatoid arthritis, scleroderma, Sjogren's syndrome, systemic lupus erythmenatosus and other diseases including sickle cell anaemia, Wilson's disease, cataracts, infertility, pulmonary contribes and beckers and expenses including sickle cell anaemia, disberterial physorythmias and expenses including sickle cell anaemia, disease, cataracts, infertility, pulmonary converse and expenses including converse and expenses including converse and expenses including converse and expenses including converse malaborption syndrome, hypercholesterolema, cancers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel human transporter and ion channel proteins useful for treating and preventing transport, neurological, muscle and immunological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      psoriasis and viral, bacterial, fungal, helminthic and protozoal infections. TRICH DNA is useful in gene therapy and in diagnostic
                                                                                                                                                                                                                                                                                                                      Reddy R,
Gandhi AR;
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0; Mismatches 221;
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Yue H, Nguyen DB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 5; Page 151-152; 160pp; English.
                                                                                                                                 2000US-0176083.
2000US-0177332.
2000US-0178572.
2000US-0179758.
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Best Local Similarity 44.3%;
Matches 176; Conservative
                                                                22-DEC-2000; 2000WO-US35095
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                                                                                                                                                                                                                                                                   (INCY-) INCYTE GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                           fang YT, Khan FA;
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                                                                                                                                    14-JAN-2000;
21-JAN-2000;
28-JAN-2000;
02-FEB-2000;
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                                  1975 agaagcacctgaggcaggagccagggacccagccctacaacatcagagaagactccattc 2034
                                                                                                        2035 tggaccaaaaggttgccctgctcaaggcataatggggccacccgtgggcatccacagttt 2094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid representing the human tumor suppressor gene TSG16, useful e.g. for diagnosis and treatment of tumors, inflammatory and
                                                                                                                                                                                                                                                                                                                                                                                                                   Tumour suppressor gene 16; TSG16; human; immune response modulator; inflammatory response modulator; signal transduction activator; cytokine inhibitor; gene therapy; anticancer; anti-inflammatory; autoimmune disorder; infection; chromosome 16q24.3;
                                                                       656 ttcatctgctgtcagcagaccacgaggaggagggggaacacacatggagaatcccttttg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 cgtgccaaggactaccacaagaagaatgagctcctgcagctcctgcagctgaagcagtcg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9063 BP; 2492 A; 2546 C; 2654 G; 1371 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kochetkova M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                               2095 gcagggtgttccggaaggttcttgtcactgtgattgg 2131
                                                                                                                                             716 accccagcttgaaggaagtcaccatctcactgagcgg 752
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WOME-) WOMEN'S & CHILDREN'S HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 137-145; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cellular proliferation suppressor; ds.
                                                                                                                                                                                                                                                                                                                                                                                    Human tumour suppressor gene, TSG16.
                                                                                                                                                                                                                                                                       AAH23688 standard; DNA; 9063 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunological disorders
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P-PSDB; AAB98612.
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Matches 82; Conserva
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1915 gigicotgotgicogotgacotgaaggggitocagiacitototacootggaagaagcag 1974

536 ctggctacctggcttttgaggagatcgcctccaccagttctggccaagtgttccagctgg

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Sequence 1260 BP; 287 A; 428 C; .350 G; 195 T; 0 other;

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signal sequence/mature alphal-antitrypsin (AAT). The protein is used to exemplify the invention. The specification describes a method for producing mature heterologous protein in monocotyledonous plant cells. The method comprises transforming the cells with a chimeric gene comprising a monocotyledon transcription regulator, inducible either during seed maturation or by adding/removing a small molecule, DNA encoding the heterologous protein, and DNA encoding a signal peptide, with the signal peptide causing secretion of the protein from the cell. The control of the signal peptide causing secretion of the protein from the cell. The control of the signal peptide causing secretion of the protein from the cell. The control of the signal peptide causing secretion of the protein from the cell. The control of the signal peptide causing characteristics, or mature exting the control of the control of the signal peptide causing emphysema, ATIII as antithrombotic and HSA as blood replacement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               present sequence encodes a fusion protein of codon-optimised RAmy3D
                                                                                                                                                                                                                                                                 Protein expression; monocotyledon plant cell; glycosylated antithrombin III; glycosylated alpha 1-antitrypsin; ART; glycosylated alpha 1-antitrypsin; ARTIII; human serum albumin; HSA; subtilisin BPN'; treatment; emphysem: antithrombotic; blood replacement; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressing mature, glycosylated proteins in monocotyledonous plant cells - from chimeric gene including signal peptide sequence, specifically therapeutic agents and industrial enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                     a
"codon-optimised RAmy3D signal sequence"
                                                                                                                                                                                                                                   Codon-optimised RAmy3D signal fused to DNA encoding mature AAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        industrial enzymes (BPN' is used in detergents)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
/note= "encodes mature AAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Pages 34 ili-iv; 53pp; English.
                                 8063 gccctgaacgccgtgcagaggatggagtg 8091
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
490 caggtggtcttcgtgctgactggggactg
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                                                                                                                          AAV41730 standard; DNA; 1260 BP
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97US-0037991.
97US-0038168.
97US-0038169.
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*tag=
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13-FEB-1997;
13-FEB-1997;
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                           AAV41730;
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                                                                         429 ccgigccaaggactaccacaagaagaatgagctccigcagciccigcagcigaagcagic 488
                                                                                                                                       819 caccgccatcttcctgccggacgaggcaagctccagcactggagaacgagctgac 878
                                                                                                                                                                 gcaggiggicittegigcigaciggggacigegigacegeacecacetiggeiaecigge 548
                                                       369 catcaaggotgocgtggaggttgccaaccccggctccttcatctacgtcttctcggatgc 428
                           Gaps
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                                                                                                                                                                                                879 gcacgacatcatcacgaagttcctggagaacgaggacaggcgctccgctagctccacct
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Length 1260;
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                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            caffeoyl-CoA 3-0-methyltranferase; lignin;
Score 41.2; DB 19;
Pred. No. 1.2;
; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Maize caffeoyl-CoA 3-0-methyltransferase cDNA.
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167..943
                                                                                                                                                                                                                                                                                                                                                                                  AAX25208 standard; cDNA; 1160 BP.
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Query Match 5.0%;
Best Local Similarity 47.6%;
Matches 121; Conservative
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transgenic plant; ss
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AAX25208
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ignin biosynthesis and/or the lignin composition of plants.
Isolated nucleic acids (see AAX25196-216) that code for proteins (see AAY05657-77) involved in lignin biosynthesis are claimed. Also claimed are recombinant expression cassettes, host cells (seeds. The claimed nucleic acids can be used to transform a plant to modulate lignin biosynthesis. A claimed method involves transforming a plant cell with a recombinant expression cassette comprising a lignin biosynthesis polynucleotide operably linked to a promoter, growing the plant cell under plant growing conditions, and inducing expression of the polynucleotide for a time sufficient to modulate (preferably increase) lignin biosynthesis in the plant. The plant lignins can be used as chemical feedstock. Plant material of increased lignin content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer content can be used as a fuel source, and in the answer can be used as a fuel source.
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protein transport; cervix cancer; dysplasia; malignancy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 561 egectecaccagttetggecaagtgttecagetggacaagcagcaggtgteggagg 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              823 catccgcttctaccgcgacttcgtgctcgtcctcaacaaggcgctcgccgacg 878
                                                                                                                                                                                                                                                                                                                  Score 40.8; DB 20; Length 1160;
Pred. No. 1.4;
0; Mismatches 122; Indels 0;
                                                                                                                                                                                                                           Decreased lignin content
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                                                                                                                                                                                                                                                                     Sequence 1160 BP; 237 A; 417 C; 311 G; 195 T; 0 other;
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                                                                                                                                                                                                                        and in the pulp and paper industry. Decreasimproves the digestibility of fodder crops.
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26..2257
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Best Local Similarity
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The nucleotide and deduced as sequences of human transducin-like enhancer of split proteins TLE-1 (AAQ62175, AAR51476), TLE-2 (AAQ62176, AAR51478) and TLE-4 (AAQ62177, AAR51479) were determined. The as sequences were compared with that of Drosophila E(spl)m9/10 protein (AAR51481). Comparison of the WD-40 domains of CCN motifs of the proteins were compared with those of the Sy40 T antigen, human c-myc, human p53, human A-myb and dorsal proteins with respect to nuclear localization site, and casein-kinase II and cdc-kinase phosphorylation sites (sequences AAR51482-96). TLE can be to study cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                135 tgtcaccggctccatgtgggacgatctgatgcaggtgatcgacggcgcctcacgcattct 194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             315 gagacaactctatgttcagggaggtggtgactgcccagaaatgagtgtgggggccatcaa
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                                                                              New human transducin-like enhancers of split protein - and associated multi-protein complexes, chimeric proteins, antibodies, nucleic acid, etc., involved in nuclear-cytoplasmic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2271 BP; 437 A; 751 C; 672 G; 411 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
4.9%; Score 40.4; DB 15;
Best Local Similarity 47.0%; Pred. No. 2.1;
Matches 125; Conservative 0; Mismatches 141;
                                                                                                                                                                                                                       Disclosure; Page 58-61; 112pp; English.
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WPI; 1994-135597/16.
P-PSDB; AAR51477.
                                                                                                                                                                     protein transport
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-SEP-1994
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The present sequence represents a new DNA sequence isolated from Pinctada fucata. The polypeptide be used as an ingredient in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            717 agccgcagccgctgctgccgctgcaggaggcgcaggtggacttggaggactcggtggcgg 776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                518 geggtgacegeacceaecctggetacetggettttgaggagategeetecaecagttetg 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 agetectgeagetectgeagetgaageagtegeagtggtettegtgetgaetggggaet 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New cDNA and e.g. vector, host cell and polypeptide - used to produce polypeptide in high yields, which is used in cosmetics
                                                                                                                                                                                                                                                                                                                                                               Sequence 2214 BP; 393 A; 451 C; 891 G; 479 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New DNA sequence isolated from Pinctada fucata.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 40.2; DI
Pred. No. 2.3;
0; Mismatches
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50..2266
/*tag= a
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                                                                                                                                                                                                                                                                         Claim 1; Page 7; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                    4.9%;
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                                                                                                                                            (MIKI-) MIKIMOTO SEIYAKU KK.
                                                                    97JP-0138461
                                                                                                          96JP-0184459
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 51.4 Matches 93; Conservative
                                                                                                                                                                                WPI; 1998-254410/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-254410/23
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JP10080285-A.
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                                                                      28-MAY-1997;
                                                                                                          15-JUL-1996;
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                                    31-MAR-1998
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                                                                                                                                                                                                                                                                                                                                                             The nucleotide and deduced aa sequences of human transducin-like enhancer of split proteins TLE-1 (AAQ45333, AAR51109), TLE-2 (AAQ45334, AAR51110), TLE-2 (AAQ45334, AAR51111) and TLE-4 (AAQ45336, AAR52953) were determined. The aa sequences were compared with that of Drosophila E(spl) m9/10 (AAR52955). Comparison of the WD-40 domains of these proteins defined the consensus residues shown in AAR52954. The CCM motifs of the proteins were compared with those of SV40 T antigen, human c-myc, human p53, human A-myb and dorsal protein with respect to nuclear localization site, and casein-kinase and cd2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ggagcgcagtctgagcagccgcagccgggtcatcgccaactatgcgctggtgcctttcca 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ccacgcacccctgtgcccctgacccccgcccagccgggctggtgggcggcagtgctac 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 135 tgtcaccggctccatgtgggacgatctgatgcaggtgatcgacggcgcctcacgcattct 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tateceetteetgaeeceaggageateageageaggtgeteeaggeegtagaaegegeeaa 357
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                                                                                                                                                                                                                                                    Transducin-like enhancer or split proteins and nucleic acids-are for treatment of disorders of cell fate or differentiation e.g. cervical cancer, breast cancer, psoriasis, baldness etc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kinase phosphorylation sites (sequences AAR52956-70).
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                                                                                                                                                                                                                                                                                                                              Disclosure; Page 91-94; 147pp; English.
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                                                     93WO-US09339
                                                                                       92US-0954813
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Matches 125; Conservative
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                                                                                                                                                                                                 WPI; 1994-135221/16.
P-PSDB; AAR51110.
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                                                     30-SEP-1993;
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                 14-APR-1994
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DB 19; Length 2214; Indels

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Unidentified.
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                                                                                                                                                                                                  invention.
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                                                                   The present sequence represents a new DNA sequence isolated from Pinctada fucata. The encoded polypeptide be used as an ingredient in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated metalloprotease thrombospondin polypeptides, useful for treating hyperproliferative disorders, cancers or autoimmune disorders
                                                                                                                                                                                                          577
                                                                                                                                                                   766 agccgcagccgctgctgccgctgcaggaggcgcaggtggacttggaggactcggtggcgg 825
                                                                                                                                                                                                                           826 acttggaggactcggtggcggacttggaggcctcggaggtcttggtggcctcggaggata 885
                                                                                                                                                                                                                                                                   886 tggaggatctgctgctgccgctgctgctgccgccgccgctgccggaggtggaggact 945
                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; METH1; METH2; anti-anglogenic; metalloprotease thrombospondin; cancer; diagnosis; hyperproliferative disorder; autoimmune disease, anglogenesis inhibitor; abnormal wound healing; inflammation; rheumatoid arthritis; psoriasis; endometrial bleeding disorder;
                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diabetic retinopathy; macula degeneration; haemangioma; detection; arterial-venous malformation; immune deficiency; ss.
                                                                                                                                                                                                         geggtgaccgcacccacctggctacctggcttttgaggagatcgcctccaccagttctg
                                                                                                                                                                                                                                               0;
                    New cDNA and e.g. vector, host cell and polypeptide - used to produce polypeptide in high yields, which is used in cosmetics
                                                                                                                             DB 19; Length 3331;
                                                                                                                                                88; Indels
                                                                                               Sequence 3331 BP; 762 A; 701 C; 1022 G; 846 T; 0 other;
                                                                                                                            4.9%; Score 40.2; DI
51.4%; Pred. No. 2.5;
tive 0; Mismatches
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                                               Claim 2; Pages 7-9; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                      AAZ32021 standard; DNA; 3331 BP.
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98US-0098539.
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                                                                                                                                               93; Conservative
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RUBEN S M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-590684/50.
                                                                                                                            Query Match
Best Local Similarity
P-PSDB; AAW56163.
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28-AUG-1998;
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(RUBE/)
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metalloprotease thrombospondin (METH) proteins METH1 and METH2
respectively. METH1 and METH2 have been found to be potent inhibitors of angiogenesis both in vitro and in vivo. They can be used for treating cancer and other disorders related to angiogenesis including abnormal wound healing, inflammation, rheumatoid arthritis, psoriasis, endometrial bleeding disorders, diabetic retinopathy, some forms of macula degeneration, haemangiomas, and arterial-venous malformations. They may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilisation (chemotaxis) of immune cells. The etiology of these immune deficiencies or disorders may be genetic, sometic, such as cancer or some autoimmune disorders, acquired (e.g. by chemotherapy or toxins), or infectious. They can also be used to treat inflammatory conditions, both chronic and acute conditions. The products can also be used for detection and diagnosis. AAS23002 to AAS2300, and AAY49511 represent sequences given in the exemplification of the present
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                                                                                   AAZ32000 and AAZ32001 encode, and AAY49501 and AAY49502 represent, human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            458 agctcctgcagctcctgcagctgaagcagtcgcaggtggtcttcgtgctgactggggact 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 3331;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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isclosure; Page 322-324; 457pp; English.
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Best Local Similarity
Matches 93; Conserv
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The present invention relates to human METH1 and METH2, (ME for metalloprotease and TH for thrombospondin; see AAB50002 and AAB50003).

The present sequence is an expressed sequence tag (EST) for METH. METH can be used for inhibiting angiogenesis in an individual, and for treating cancer, benign tumours, an ocular angiogenic disease, rheumatoid arthritis, psoriasis, delayed wound healing, endometriosis, vasculogenesis, granulations, hypertrophic scars, nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, cerebral collaterals, arteriovenous malformations, ischaemic limb angiogenesis, Osler-Webber syndrome, plaque neovascularisation, telanglectasia, haemophiliac joints, anglofibroma, thoromscular dysplasia, wound granulation, corbn's disease or atherosclerosis. METH can also be used in birth control. METH can also
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           METH1 and METH2 polynucleotides and encoded polypeptides, used to inhibit angiogensis in the treatment of disorders such as cancer, rheumatoid arthritis and psoriasis -
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4.9%; Score 40.2; DB 22; Length 3331;
Best Local Similarity 51.4%; Pred. No. 2.5;
Matches 93; Conservative 0; Mismatches 88; Indels 0;
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Fornwald JA, Terrett JA;
                                                                                                                                                                                       BETH ISRAEL DEACONESS MEDICAL CENT. IRUELA-ARISPE L.
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                                                                                                                                                                          SMITHKLINE BEECHAM CORP
                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                20-JUL-1999; 99US-0144882.
10-AUG-1999; 99US-0147823.
13-AUG-1999; 99US-0373658.
22-DEC-1999; 99US-0171503.
22-FEB-2000; 2000US-0183792.
2000WO-US14462
                                                                                                                                                                                                                       HASTINGS G A.
RUBEN S M.
JONAK Z L.
TRULLI S H.
FORNWALD J A.
                                                                                                                                                                                                                                                                                                             (TERR/) TERRETT J A.
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25-MAY-2000;
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